

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104100\_us-10-553-509- 11.szlm60.rng.

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GenCore version 5.1.9  
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4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 05:57:43 ; Search time 192.899 Seconds  
(without alignments)  
578.313 Million cell updates/sec

Title: US-10-553-509-11  
Perfect score: 16  
Sequence: 1 catcgcttggaactccg 16

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5397982

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseqn8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
1	16	catcgcttggaactccg	16	16	12	ADT02451	ADT02451 Fluorescent

3	3	16	100.0	17	2	AAT58987	Aat58987 Obesity a
3	4	16	100.0	17	14	AEC91758	Aec91758 Probe 5T-
	5	16	100.0	18	13	ADT93450	Adt93450 Fluoresce
	6	16	100.0	19	6	ABK50102	Abk50102 Allele sp
	7	16	100.0	20	13	ADT93449	Adt93449 Fluoresce
	8	16	100.0	21	4	AAF96885	Aaf96885 Human gen
	9	16	100.0	25	12	ADO26525	Ado26525 Novel hyb
	10	16	100.0	26	6	ABL40567	Abl40567 Primer #7
	11	16	100.0	34	13	ADT93453	Adt93453 Human bet
	12	15.6	100.0	21	3	AAC73164	Aac73164 SNP flank
	13	15.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
	14	15.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
	15	15	93.8	15	13	ADT93452	Adt93452 Fluoresce
3	16	15	93.8	18	14	AEC91756	Aec91756 Probe 3T-
3	17	14.4	90.0	17	2	AAT58988	Aat58988 Obesity a
	18	14.4	90.0	17	2	AAT58990	Aat58990 Obesity a
	19	14.4	90.0	19	13	ADT93446	Adt93446 Fluoresce
	20	14.4	90.0	21	14	AEC91760	Aec91760 Probe 3T-
	21	14.4	90.0	25	6	ABL40568	Abl40568 Primer #8
	22	14.4	90.0	25	12	ADO26526	Ado26526 Novel hyb
	23	14.4	90.0	34	13	ADT93454	Adt93454 Human bet
	24	14.4	90.0	41	6	ABK50104	Abk50104 Sense str
3	25	14	87.5	14	13	ADU50896	Adu50896 Human bet
3	26	14	87.5	14	14	ADZ42342	Adz42342 FAM probe
	27	14	87.5	21	4	AAF96886	Aaf96886 Human gen
	28	14	87.5	51	4	AAH90342	Aah90342 Human clo
	29	14	87.5	51	4	AAH90341	Aah90341 Human clo
	30	13.6	85.0	34	2	AAV33317	Aav33317 Anti-CD23
	31	13.4	83.8	16	13	ADT93445	Adt93445 Fluoresce
3	32	13.4	83.8	25	4	AAC89164	Aac89164 Sample DN
	33	13.4	83.8	33	2	AAQ87254	Aaq87254 Primer fo
	34	13.4	83.8	35	2	AAV24264	Aav24264 Chimeric
	35	13.4	83.8	35	2	AAX00108	Aax00108 Human ant
	36	13.4	83.8	35	3	AAZ58889	Aaz58889 PCR prime
	37	13.4	83.8	35	4	AAF69217	Aaf69217 Chimeric
	38	13.4	83.8	35	4	AAF69105	Aaf69105 Chimeric
	39	13.4	83.8	35	4	AAH75082	Aah75082 Nucleotid
	40	13.4	83.8	35	4	AAH76620	Aah76620 Chimeric
	41	13.4	83.8	35	5	AAH74261	Aah74261 Nucleotid
	42	13.4	83.8	35	5	AAF69161	Aaf69161 Chimeric
	43	13.4	83.8	35	6	ABL94797	Abl94797 Joint dis
	44	13.4	83.8	35	10	ABT31649	Abt31649 Angiogene
	45	13.4	83.8	35	12	ADO33818	Ado33818 Parathyro

ALIGNMENTS

```

ESULT 1
DT93451
D  ADT93451 standard; DNA; 16 BP.
X
C  ADT93451;
X
F  13-JAN-2005  (first entry)
X
E  Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 11.
X
W  SNP detection; beta3 adrenaline receptor; ss; probe.
X
S  Homo sapiens.
X
H  Key          Location/Qualifiers
F  modified_base 1
F                      /*tag= a
F                      /mod_base= OTHER
F                      /note= "OTHER = Linked to BODIPY FL group"
F  modified_base 16
F                      /*tag= b
F                      /mod_base= OTHER

```

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 2; SEQ ID NO 11; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the fluorescent-labelled probe (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline receptor (B3AR) T190 variant DNA.

Sequence 16 BP; 2 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCG 16  
|||||||  
1 CATCGCCTGGACTCCG 16

RESULT 2

AT58989

AAT58989 standard; DNA; 17 BP.

AAT58989;

04-AUG-1997 (first entry)

Obesity and type II diabetes mellitus diagnosis nucleic acid probe.

Hybridisation; polymerase chain reaction; beta3-adrenergic receptor; beta3AR; ss.

Synthetic.

WO9636641-A1.

21-NOV-1996.

17-MAY-1996; 96WO-US007218.

19-MAY-1995; 95US-00446530.

Shuldiner AR, Walston J, Silver K, Roth J;  
WPI; 1997-012034/01.

New isolated beta3-adrenergic receptor mutation - used to develop prods.  
for the diagnosis and treatment of type II diabetes and/or obesity.

Claim 17; Page 42; 51pp; English.

The present sequence is a nucleic acid probe used in a method for  
diagnosis of a subject having or at risk of having type II diabetes  
mellitus and/or obesity. The method involves contacting a target nucleic  
acid of a sample from the subject with a nucleic acid probe (preferably  
the present sequence or that in AAT58990) that detects a mutation in the  
beta3-adrenergic receptor (beta3AR) gene. The present sequence can also  
be used in the treatment of subjects having or at risk of having type II  
diabetes and/or obesity

Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 CATCGCCTGGACTCCG 16
  |||||
1 CATCGCCTGGACTCCG 16
```

### RESULT 3

AT58987/c

AAT58987 standard; DNA; 17 BP.

AAT58987;

04-AUG-1997 (first entry)

Obesity and type II diabetes mellitus diagnosis target nucleic acid.

Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;  
beta3AR; ss.

Synthetic.

WO9636641-A1.

21-NOV-1996.

17-MAY-1996; 96WO-US007218.

19-MAY-1995; 95US-00446530.

(UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.

Shuldiner AR, Walston J, Silver K, Roth J;

WPI; 1997-012034/01.

New isolated beta3-adrenergic receptor mutation - used to develop prods.  
for the diagnosis and treatment of type II diabetes and/or obesity.

Claim 16; Page 42; 51pp; English.

The present sequence is a target nucleic acid detected in a method for  
diagnosis of a subject having or at risk of having type II diabetes  
mellitus and/or obesity. The method involves contacting a target nucleic  
acid of a sample from the subject (preferably the present sequence or  
that in AAT58988) with a nucleic acid probe that detects a mutation in  
the beta3-adrenergic receptor (beta3AR) gene

2 Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCG 16  
 |||||  
 17 CATCGCCTGGACTCCG 2

ESULT 4  
 EC91758/c

D AEC91758 standard; DNA; 17 BP.  
 X  
 C AEC91758;  
 X  
 T 01-DEC-2005 (first entry)  
 X  
 E Probe 5T-B3AR-w-IMS-R2-17 SEQ ID NO:34.  
 X  
 W DNA detection; SNP detection; probe; ss.  
 X  
 S Synthetic.  
 X  
 N JP2005261354-A.  
 X  
 D 29-SEP-2005.  
 X  
 F 19-MAR-2004; 2004JP-00080974.  
 X  
 R 19-MAR-2004; 2004JP-00080974.  
 X  
 A (KYOT-) KYOTO DAIICHI KAGAKU KK.  
 X  
 I Inose K;  
 X  
 R WPI; 2005-662138/68.  
 X  
 T Detecting target nucleic acid, involves detecting target based on change  
 T of fluorescence intensity due to formation or dissociation of hybrid of  
 T target nucleic acid and hybridization probe having 5-carboxy fluorescein.  
 X  
 S Example 10; SEQ ID NO 34; 28pp; Japanese.  
 X  
 C The invention relates to a method (M1) for detecting a target nucleic  
 C acid. (M1) involves measuring the change of fluorescence intensity due to  
 C formation or dissociation of the hybrid of the hybridization probe  
 C comprising a labeled terminal portion, and a target nucleic acid, and  
 C detecting the target nucleic acid based on the change, where the  
 C hybridization probe is labeled using the fluorescent pigment chosen from  
 C 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora  
 C -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-  
 C dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),  
 C 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxylaceto  
 C hydrazide (Cascade blue). Also described: (1) a real-time PCR method  
 C (M2), which involves carrying out real-time PCR using the hybridization  
 C probe labeled with the fluorescent pigment, where the hybridization probe  
 C is the probe labeled at its terminal with the fluorescent pigment chosen  
 C from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-  
 C curve analysis (M3), which involves using the hybridization probe labeled  
 C with the fluorescent pigment, where the hybridization probe is the probe  
 C labeled at its terminal with the fluorescent pigment chosen from TAMRA,  
 C BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a  
 C target nucleic acid. (M1)-(M3) are useful for detecting mutations in a  
 C target nucleic acid and single nucleotide polymorphisms (SNPs), and in  
 C measurement of the ratio of normal type DNA and variant DNA. (M1) enables  
 C detection of the nucleic acid by fluorescent detection method, easily and  
 C cost effectively. The present sequence represents a probe used in an  
 C example from the present invention

2 Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCG 16  
|||  
O 17 CATCGCCTGGACTCCG 2

ESULT 5

DT93450

O ADT93450 standard; DNA; 18 BP.

X

C ADT93450;

X

T 13-JAN-2005 (first entry)

X

E Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.

X

N SNP detection; beta3 adrenaline receptor; ss; probe.

X

S Homo sapiens.

X

H Key Location/Qualifiers

T modified\_base 1

T /\*tag= a

T /mod\_base= OTHER

T /note= "OTHER = Linked to BODIPY FL group"

T modified\_base 18

T /\*tag= b

T /mod\_base= OTHER

T /note= "OTHER = Optionally linked to P group"

X

N WO2004092385-A1.

X

O 28-OCT-2004.

X

F 16-APR-2004; 2004WO-JP005525.

X

R 18-APR-2003; 2003JP-00114381.

X

A (ARKR-) ARKRAY INC.

X

I Hirai M;

X

R WPI; 2004-784610/77.

X

T Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
T receptor gene having single nucleotide polymorphism, labeled at terminal  
T with fluorescent dye and shows decrease in fluorescence of fluorescent  
T dye upon hybridization.

X

S Claim 2; SEQ ID NO 10; 31pp; Japanese.

X

C The invention relates to a novel nucleic acid probe which is labelled at  
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
C of the fluorescent dye is observed upon hybridisation. The probe  
C comprises a base sequence derived from a fully defined sequence of 1227  
C nucleotides as given in the specification and being labelled at the 3' or  
C 5' end with a fluorescent dye. The probe of the invention may be useful  
C for detecting a mutation or single nucleotide polymorphism (SNP) in the  
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
C contamination of the amplified product is prevented and the process is  
C automated. The current sequence is that of the fluorescent-labelled probe  
C (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline  
C receptor (B3AR) T190 variant DNA.

2 Sequence 10 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCG 16  
|||  
o 1 CATCGCCTGGACTCCG 16

ESULT 6  
BK50102

o ABK50102 standard; DNA; 19 BP.  
X  
o ABK50102;  
X  
F 15-JUL-2002 (first entry)  
X  
E Allele specific hybridisation probe.  
X  
W Optimal reagent oligonucleotide; target nucleic acid evaluation;  
W target feature; exclusion value; ranking value; sequence window;  
W hybridisation; probe; ss.  
X  
S Synthetic.  
X  
W WO200229379-A2.  
X  
o 11-APR-2002.  
X  
F 04-OCT-2001; 2001WO-US031037.  
X  
R 04-OCT-2000; 2000US-0237383P.  
X  
A (CELA-) CELADON LAB INC.  
X  
I Peterson RJ;  
X  
R WPI; 2002-340129/37.  
X  
F Determining an optimal reagent oligonucleotide for evaluating a target  
F nucleic acid having a target feature, involves defining a set of  
F exclusion values and/or ranking values specific to a biochemical method.  
X  
S Example; Fig 2A; 91pp; English.  
X  
o The present invention relates to a new method for determining an optimal  
o reagent oligonucleotide for evaluating a target nucleic acid having a  
o target feature. The method comprises defining a set of exclusion values  
o and/or ranking values specific to the method, defining a sequence window  
o adjacent to the target, and generating candidate reagent oligonucleotides  
o complementary to the sense and/or antisense strands of the target within  
o the window. The method can be used for determining an optimal reagent  
o oligonucleotide sequence for use in a biochemical method for evaluating a  
o target nucleic acid sequence having a target feature. The present nucleic  
o acid sequence represent an allele specific hybridisation probe that was  
o used in the methods of the invention in numbering systems  
X  
2 Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCG 16  
|||  
o 3 CATCGCCTGGACTCCG 18

```

> ADT93449 standard; DNA; 20 BP.
> ADT93449;
> 13-JAN-2005 (first entry)
> Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.
> SNP detection; beta3 adrenaline receptor; ss; probe.
> Homo sapiens.
>
> Key Location/Qualifiers
> modified_base 1
> /*tag= a
> /mod_base= OTHER
> /note= "OTHER = Linked to BODIPY FL group"
> modified_base 20
> /*tag= b
> /mod_base= OTHER
> /note= "OTHER = Linked to P group"
>
> WO2004092385-A1.
>
> 28-OCT-2004.
>
> 16-APR-2004; 2004WO-JP005525.
>
> 18-APR-2003; 2003JP-00114381.
>
> (ARKR-) ARKRAY INC.
>
> Hirai M;
>
> WPI; 2004-784610/77.
>
> Nucleic acid probe useful for detecting mutation in beta3 adrenaline
> receptor gene having single nucleotide polymorphism, labeled at terminal
> with fluorescent dye and shows decrease in fluorescence of fluorescent
> dye upon hybridization.
>
> Claim 2; SEQ ID NO 9; 31pp; Japanese.
>
> The invention relates to a novel nucleic acid probe which is labelled at
> a terminal with a fluorescent dye, whereby a decrease in the fluorescence
> of the fluorescent dye is observed upon hybridisation. The probe
> comprises a base sequence derived from a fully defined sequence of 1227
> nucleotides as given in the specification and being labelled at the 3' or
> 5' end with a fluorescent dye. The probe of the invention may be useful
> for detecting a mutation or single nucleotide polymorphism (SNP) in the
> beta3 adrenaline receptor (B3AR) gene. The probe is effective in
> detecting a B3AR Trp64Arg mutation within a short time whilst risk of
> contamination of the amplified product is prevented and the process is
> automated. The current sequence is that of the fluorescent-labelled probe
> (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
> receptor (B3AR) T190 variant DNA.
>
> Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

```

```

Query Match 100.0%; Score 16; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

> 1 CATCGCCTGGACTCCG 16
> |||||
> 1 CATCGCCTGGACTCCG 16

```



AAF96885;

18-NOV-2004 (revised)

06-JUN-2001 (first entry)

Human gene single nucleotide polymorphism #1646.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.

Homo sapiens.

Unidentified.

Key Location/Qualifiers  
variation 11  
/\*tag= a  
/standard\_name= "Single nucleotide polymorphism"

WO200118250-A2.

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.

26-JUL-2000; 2000US-0220947P.

16-AUG-2000; 2000US-0225724P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;

WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.

Example; Page 159; 242pp; English.

The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPs shown in the specification

Revised record issued on 18-NOV-2004 : The variantion feature was incorrectly given a captial V

Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCG 16

|||||||

4 CATCGCCTGGACTCCG 19

ESULT 9  
DO26525.  
D ADO26525 standard; DNA; 25 BP.  
K  
C ADO26525;  
K  
F 12-AUG-2004 (first entry)  
K  
E Novel hybridisation detection-related oligonucleotide SeqID1.  
K  
W hybridisation detection; immobilised probe; AC impedance;  
W foetal genome analysis; ss.  
K  
S Unidentified.  
K  
N WO2004044570-A1.  
K  
D 27-MAY-2004.  
K  
F 30-SEP-2003; 2003WO-JP012499.  
K  
R 14-NOV-2002; 2002JP-00331059.  
K  
A (TOYA-) TOYAMA PREFECTURE.  
A (COSE-) COSEL CO LTD.  
A (TATE-) TATEYAMA KAGAKU IND CO LTD.  
A (TOXX ) TOYO KAKO CO LTD.  
K  
I Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;  
I Nakagawa A, Mizuhara T, Mizushima M, Nakada M;  
K  
R WPI; 2004-420427/39.  
K  
F Detection of hybridization of an immobilized probe to a target nucleic  
F acid by measuring AC impedance across the carrier surface for specific  
F gene detection in investigation and diagnosis of disease.  
K  
S Example; SEQ ID NO 1; 33pp; Japanese.  
K  
C This invention relates to a novel method of detecting hybridisation of an  
C immobilised probe to a target nucleic acid using measurement of AC  
C impedance. Detection of specific genes and gene sequences in nucleic acid  
C samples (such as samples of genomic DNA) may be useful for diagnosis,  
C prediction and prevention of genetic disorders and analysis of foetal  
C genome. Hybridisation is detected with high accuracy and sensitivity  
C without the use of dyes. The present sequence is that of an  
C oligonucleotide which was used in the exemplification of the invention.  
K  
Q Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 16; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 1 CATCGCCTGGACTCCG 16  
|||  
C 6 CATCGCCTGGACTCCG 21

ESULT 10  
3L40567  
D ABL40567 standard; DNA; 26 BP.  
K  
C ABL40567;  
K  
F 17-JUN-2002 (first entry)  
K  
E Primer #7 used in a base polymorphism detection method.  
K  
W Polymorphism; nucleic acid detection; endonuclease; probe; ABBP2.

.. hybridization, PCR primer, etc.

X  
S Synthetic.  
X  
N JP2002034598-A.  
X  
D 05-FEB-2002.  
X  
F 27-JUL-2000; 2000JP-00226912.  
X  
R 27-JUL-2000; 2000JP-00226912.  
X  
A (TOYM ) TOYOBO KK.  
X  
R WPI; 2002-298820/34.  
X  
I Detection of base polymorphism.  
X  
S Disclosure; Page 10; 10pp; Japanese.  
X  
C The invention relates to a method for detecting base polymorphism. The  
C method involves (1) amplifying the nucleic acid fragment containing base  
C polymorphism of the specific nucleic acid sequence; (2) hybridising the  
C amplified nucleic acid with at least two polymorphism-specific probes;  
C (3) treating with RNA-selective cleavage endonuclease; (4) measuring  
C detecting signals of each probe; and (5) identifying polymorphism by the  
C ratio of each detecting signals. The probe can be used for detecting base  
C polymorphism. The present sequence represents a PCR primer used in the  
C course of the invention  
X  
2 Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 CATCGCCTGGACTCCG 16  
|||  
O 9 CATCGCCTGGACTCCG 24

RESULT 11  
DT93453  
D ADT93453 standard; DNA; 34 BP.  
X  
C ADT93453;  
X  
I 13-JAN-2005 (first entry)  
X  
E Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.  
X  
W single nucleotide polymorphism; SNP; SNP detection;  
W beta3 adrenaline receptor; ds.  
X  
S Homo sapiens.  
X  
H Key Location/Qualifiers  
I variation replace(19,C)  
I /\*tag= a  
I /standard\_name= "Single nucleotide polymorphism"  
X  
N WO2004092385-A1.  
X  
D 28-OCT-2004.  
X  
F 16-APR-2004; 2004WO-JP005525.  
X  
R 18-APR-2003; 2003JP-00114381.  
X  
A (ARKR-) ARKRAY INC.  
v

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Example 1; Fig 1; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment of the invention.

Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 13; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 CATCGCCTGGACTCCG 16
  |||||
12 CATCGCCTGGACTCCG 27
```

#### ESULT 12

AC73164

AAC73164 standard; DNA; 21 BP.

AAC73164;

02-FEB-2001 (first entry)

SNP flanking sequence #24 used in multiplexing PCR/SBE assay.

Oligonucleotide array; genotyping; single base extension reaction; SBE; polymorphic locus; single nucleotide polymorphism; ss.

Unidentified.

WO200058516-A2.

05-OCT-2000.

27-MAR-2000; 2000WO-US008069.

26-MAR-1999; 99US-0126473P.

23-JUN-1999; 99US-0140359P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

(AFFY-) AFFYMETRIX INC.

Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ; Ryder T, Sklar P;

WPI; 2000-656171/63.

Universal array of oligonucleotides tags attached to a solid substrate along with locus-specific tagged oligonucleotides useful in genotyping using single base extension reactions.

The present invention relates to an oligonucleotide array comprising oligonucleotide tags fixed to a solid substrate. The oligonucleotide array is useful for genotyping a nucleic acid sample at one or more loci via single base extension (SBE) reactions. A pair of primers is used to amplify a polymorphic locus in a sample e.g. a single nucleotide polymorphism (SNP). The present sequence is one such polymorphic locus used in the present invention. The amplified nucleic acid product is then used as a template in a SBE reaction with an extension primer. The SBE reaction products are used to form the oligonucleotide array. Note: This sequence includes a SNP represented by the degenerate codon in the sequence

Sequence 21 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 1 Other;

Query Match 100.0%; Score 16; DB 3; Length 21;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCG 16  
|||||||:|||||||  
4 CATGCCYGGACTCCG 19

RESULT 13

AA04696

AAA04696 standard; DNA; 29 BP.

AAA04696;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene ADRB3.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999; 99EP-00250150.

07-MAY-1998; 98US-0084641P.

03-MAY-1999; 99US-00304232.

(AFFY-) AFFYMETRIX INC.

(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

Disclosure; Page 45; 53pp; English.

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be

used for association studies for hypertension, and in hypertension  
diagnostic assays. Where the polymorphisms have strong correlation with  
hypertension, within a gene, they are likely to have a causative role in  
hypertension. This information can be used to find the precise role of a  
polymorphism in the disease, and this can be used to identify potential  
drugs which combat the disease. The polymorphisms can be tested for  
association with other diseases e.g. agammaglobulinemia, diabetes  
insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
syndrome, Fabrys disease, familial hypercholesterolemia, polycystic  
kidney disease, hereditary spherocytosis, von Willebrands disease,  
tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial  
colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
acute intermittent porphyria. The polymorphic forms can also be used in  
forensics to identify individuals

Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 16; DB 3; Length 29;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCG 16  
||||||:|||||||  
8 CATCGCCYGGACTCCG 23

ESULT 14

3K50101

ABK50101 standard; DNA; 41 BP.

ABK50101;

15-JUL-2002 (first entry)

Nucleic acid sequence used for sequence formatting.

Optimal reagent oligonucleotide; target nucleic acid evaluation;  
target feature; exclusion value; ranking value; sequence window;  
sequence formatting; ds.

Synthetic.

WO200229379-A2.

11-APR-2002.

04-OCT-2001; 2001WO-US031037.

04-OCT-2000; 2000US-0237383P.

(CELA-) CELADON LAB INC.

Peterson RJ;

WPI; 2002-340129/37.

Determining an optimal reagent oligonucleotide for evaluating a target  
nucleic acid having a target feature, involves defining a set of  
exclusion values and/or ranking values specific to a biochemical method.

Example; Fig 1B; 91pp; English.

The present invention relates to a new method for determining an optimal  
reagent oligonucleotide for evaluating a target nucleic acid having a  
target feature. The method comprises defining a set of exclusion values  
and/or ranking values specific to the method, defining a sequence window  
adjacent to the target, and generating candidate reagent oligonucleotides  
complementary to the sense and/or antisense strands of the target within  
the window. The method can be used for determining an optimal reagent  
oligonucleotide sequence for use in a biochemical method for evaluating a  
target nucleic acid sequence having a target feature. The present nucleic

invention for nucleic acid sequence formatting  
Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;  
Query Match 100.0%; Score 16; DB 6; Length 41;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 CATCGCCTGGACTCCG 16  
|||||:|||||  
14 CATCGCCYGGACTCCG 29

ESULT 15  
DT93452  
ADT93452 standard; DNA; 15 BP.  
ADT93452;  
13-JAN-2005 (first entry)

[tart](#) | [next page](#)

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104100\_us-10-553-509-12.szlm60.rng.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104100\_us-10-53-509-12.szlm60.rng.

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GenCore version 5.1.9  
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4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 05:57:43 ; Search time 180.843 Seconds  
(without alignments)  
578.313 Million cell updates/sec

Title: US-10-553-509-12  
Effect score: 15  
Sequence: 1 catcgcttgactcc 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5397982

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:  
14: geneseqn2005s:  
15: geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	15	100	15	10	10000000	10000000	



2	15	100.0	17	2	AAT58989	Aat58989 Obesity a
3	15	100.0	17	2	AAT58987	Aat58987 Obesity a
4	15	100.0	17	14	AEC91758	Aec91758 Probe 5T-
5	15	100.0	18	13	ADT93450	Adt93450 Fluoresce
6	15	100.0	19	6	ABK50102	Abk50102 Allele sp
7	15	100.0	20	13	ADT93449	Adt93449 Fluoresce
8	15	100.0	21	4	AAF96885	Aaf96885 Human gen
9	15	100.0	25	12	ADO26525	Ado26525 Novel hyb
10	15	100.0	26	6	ABL40567	Abl40567 Primer #7
11	15	100.0	34	13	ADT93453	Adt93453 Human bet
12	14.6	100.0	21	3	AAC73164	Aac73164 SNP flank
13	14.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
14	14.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
15	14	93.3	18	14	AEC91756	Aec91756 Probe 3T-
16	14	93.3	51	4	AAH90342	Aah90342 Human clo
17	14	93.3	51	4	AAH90341	Aah90341 Human clo
18	13.4	89.3	16	13	ADT93445	Adt93445 Fluoresce
19	13.4	89.3	17	2	AAT58988	Aat58988 Obesity a
20	13.4	89.3	17	2	AAT58990	Aat58990 Obesity a
21	13.4	89.3	19	13	ADT93446	Adt93446 Fluoresce
22	13.4	89.3	21	14	AEC91760	Aec91760 Probe 3T-
23	13.4	89.3	25	4	AAC89164	Aac89164 Sample DN
24	13.4	89.3	25	6	ABL40568	Abl40568 Primer #8
25	13.4	89.3	25	12	ADO26526	Ado26526 Novel hyb
26	13.4	89.3	33	2	AAQ87254	Aaq87254 Primer fo
27	13.4	89.3	34	13	ADT93454	Adt93454 Human bet
28	13.4	89.3	35	2	AAV24264	Aav24264 Chimeric
29	13.4	89.3	35	2	AAX00108	Aax00108 Human ant
30	13.4	89.3	35	3	AAZ58889	Aaz58889 PCR prime
31	13.4	89.3	35	4	AAF69217	Aaf69217 Chimeric
32	13.4	89.3	35	4	AAF69105	Aaf69105 Chimeric
33	13.4	89.3	35	4	AAH75082	Aah75082 Nucleotid
34	13.4	89.3	35	4	AAH76620	Aah76620 Chimeric
35	13.4	89.3	35	5	AAH74261	Aah74261 Nucleotid
36	13.4	89.3	35	5	AAF69161	Aaf69161 Chimeric
37	13.4	89.3	35	6	ABL94797	Abl94797 Joint dis
38	13.4	89.3	35	10	ABT31649	Abt31649 Angiogene
39	13.4	89.3	35	12	ADO33818	Ado33818 Parathyro
40	13.4	89.3	39	2	AAQ35923	Aaq35923 Human/mon
41	13.4	89.3	39	2	AAT92223	Aat92223 Monkey/hu
42	13.4	89.3	39	2	AAT62895	Aat62895 Human or
43	13.4	89.3	39	2	AAT95148	Aat95148 Human or
44	13.4	89.3	39	2	AAV05670	Aav05670 Human/mon
45	13.4	89.3	39	2	AAV05670	Aav05670 Human/mon

# ALIGNMENTS

```

ESULT 1
DT93452
O ADT93452 standard; DNA; 15 BP.
K
C ADT93452;
K
T 13-JAN-2005 (first entry)
K
E Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 12.
K
W SNP detection; beta3 adrenaline receptor; ss; probe.
K
S Homo sapiens.
K
H Key Location/Qualifiers
T modified_base 1
T /*tag= a
T /mod_base= OTHER
T /note= "OTHER = Linked to BODIPY FL group"
T modified_base 15
T /*tag= b
T /mod_base= OTHER

```

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai, M.

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 2; SEQ ID NO 12; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the fluorescent-labelled probe (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline receptor (B3AR) T190 variant DNA.

Sequence 15 BP; 2 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 CATCGCCTGGACTCC 15
  |||||
1 CATCGCCTGGACTCC 15
    
```

## ESULT 2

DT93451

ADT93451 standard; DNA; 16 BP.

ADT93451;

13-JAN-2005 (first entry)

Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 11.

SNP detection; beta3 adrenaline receptor; ss; probe.

Homo sapiens.

Key	Location/Qualifiers
modified_base	1
	/*tag= a
	/mod_base= OTHER
	/note= "OTHER = Linked to BODIPY FL group"
modified_base	16
	/*tag= b
	/mod_base= OTHER
	/note= "OTHER = optionally linked to B group"

N  
X  
D  
X  
F  
X  
R  
X  
A  
X  
I  
X  
R  
X  
F  
F  
F  
X  
S  
X  
C  
C  
C  
C  
C  
C  
C  
C  
C  
C  
C  
C  
X  
2  
  
Y  
o  
  
E  
X  
N  
N  
X  
S  
X  
N  
X  
D  
X  
F  
X  
R  
X  
A

WO2004092385-A1.  
28-OCT-2004.  
16-APR-2004; 2004WO-JP005525.  
18-APR-2003; 2003JP-00114381.  
(ARKR-) ARKRAY INC.  
Hirai M;  
WPI; 2004-784610/77.  
Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
receptor gene having single nucleotide polymorphism, labeled at terminal  
with fluorescent dye and shows decrease in fluorescence of fluorescent  
dye upon hybridization.  
Claim 2; SEQ ID NO 11; 31pp; Japanese.  
The invention relates to a novel nucleic acid probe which is labelled at  
a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
of the fluorescent dye is observed upon hybridisation. The probe  
comprises a base sequence derived from a fully defined sequence of 1227  
nucleotides as given in the specification and being labelled at the 3' or  
5' end with a fluorescent dye. The probe of the invention may be useful  
for detecting a mutation or single nucleotide polymorphism (SNP) in the  
beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
contamination of the amplified product is prevented and the process is  
automated. The current sequence is that of the fluorescent-labelled probe  
(SEQ ID 5) of the invention which was targeted to human beta3 adrenaline  
receptor (B3AR) T190 variant DNA.  
Sequence 16 BP; 2 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CATCGCCTGGACTCC 15  
|||||||  
1 CATCGCCTGGACTCC 15

ESULT 3  
AT58989  
AAT58989 standard; DNA; 17 BP.  
AAT58989;  
04-AUG-1997 (first entry)  
Obesity and type II diabetes mellitus diagnosis nucleic acid probe.  
Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;  
beta3AR; ss.  
Synthetic.  
WO9636641-A1.  
21-NOV-1996.  
17-MAY-1996; 96WO-US007218.  
19-MAY-1995; 95US-00446530.  
(UNIV. OF TORONTO HOSPITAL MED

I Shuldiner AR, Walston J, Silver K, Roth J;  
K  
R WPI; 1997-012034/01.  
K  
F New isolated beta3-adrenergic receptor mutation - used to develop prods.  
F for the diagnosis and treatment of type II diabetes and/or obesity.  
K  
S Claim 17; Page 42; 51pp; English.  
K  
C The present sequence is a nucleic acid probe used in a method for  
C diagnosis of a subject having or at risk of having type II diabetes  
C mellitus and/or obesity. The method involves contacting a target nucleic  
C acid of a sample from the subject with a nucleic acid probe (preferably  
C the present sequence or that in AAT58990) that detects a mutation in the  
C beta3-adrenergic receptor (beta3AR) gene. The present sequence can also  
C be used in the treatment of subjects having or at risk of having type II  
C diabetes and/or obesity  
K  
Q Sequence 17, BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15  
| | | | | | | | | | | | | | |  
O 1 CATCGCCTGGACTCC 15

ESULT 4  
AT58987/c  
O AAT58987 standard; DNA; 17 BP.  
K  
C AAT58987;  
K  
F 04-AUG-1997 (first entry)  
K  
E Obesity and type II diabetes mellitus diagnosis target nucleic acid.  
K  
W Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;  
W beta3AR; ss.  
K  
S Synthetic.  
K  
N WO9636641-A1.  
K  
O 21-NOV-1996.  
K  
F 17-MAY-1996; 96WO-US007218.  
K  
R 19-MAY-1995; 95US-00446530.  
K  
A (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.  
K  
I Shuldiner AR, Walston J, Silver K, Roth J;  
K  
R WPI; 1997-012034/01.  
K  
F New isolated beta3-adrenergic receptor mutation - used to develop prods.  
F for the diagnosis and treatment of type II diabetes and/or obesity.  
K  
S Claim 16; Page 42; 51pp; English.  
K  
C The present sequence is a target nucleic acid detected in a method for  
C diagnosis of a subject having or at risk of having type II diabetes  
C mellitus and/or obesity. The method involves contacting a target nucleic  
C acid of a sample from the subject (preferably the present sequence or  
C that in AAT58988) with a nucleic acid probe that detects a mutation in  
C the beta3-adrenergic receptor (beta3AR) gene  
v

Query Match 100.0%; Score 15; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

y      1 CATCGCCTGGACTCC 15
      |||||
c      17 CATCGCCTGGACTCC 3

```

RESULT 5

EC91758/c

2 AEC91758 standard; DNA; 17 BP.

X  
C AEC91758;

T 01-DEC-2005 (first entry)

E Probe 5T-B3AR-w-IMS-R2-17 SEO ID NO:34.

W DNA detection; SNP detection; probe; ss.

3 Synthetic.

N JP2005261354-A.

29-SEP-2005.

F 19-MAR-2004; 2004JP-00080974.

R 19-MAR-2004; 2004JP-00080974.

A (KYOT-) KYOTO DAIICHI KAGAKU KK.

I Inose K;

R WPI; 2005-662138/68.

Detecting target nucleic acid, involves detecting target based on change of fluorescence intensity due to formation or dissociation of hybrid of target nucleic acid and hybridization probe having 5-carboxy fluorescein.

5 Example 10; SEQ ID NO 34; 28pp; Japanese.

The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxyl]aceto hydrazide (Cascade blue). Also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a probe used in an example from the present invention.

Sequence 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000

Query Match 100.0%; Score 15; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCC 15  
|||||||  
17 CATCGCCTGGACTCC 3

RESULT 6  
DT93450

ADT93450 standard; DNA; 18 BP.  
ADT93450;  
13-JAN-2005 (first entry)  
Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.  
SNP detection; beta3 adrenaline receptor; ss; probe.  
Homo sapiens.  
Key Location/Qualifiers  
modified\_base 1  
/\*tag= a  
/mod\_base= OTHER  
/note= "OTHER = Linked to BODIPY FL group"  
modified\_base 18  
/\*tag= b  
/mod\_base= OTHER  
/note= "OTHER = Optionally linked to P group"  
WO2004092385-A1.  
28-OCT-2004.  
16-APR-2004; 2004WO-JP005525.  
18-APR-2003; 2003JP-00114381.  
(ARKR-) ARKRAY INC.  
Hirai M;  
WPI; 2004-784610/77.  
Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 2; SEQ ID NO 10; 31pp; Japanese.  
The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the fluorescent-labelled probe (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline receptor (B3AR) T190 variant DNA.

Sequence 18 BP: 2 A, 7 G, 5 C, 2 T, 0 U, 0 Other.

Query Match 100.0%; Score 15; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15  
| | | | | | | | | | | | | | | |  
C 1 CATCGCCTGGACTCC 15

ESULT 7  
3K50102

C ABK50102 standard; DNA; 19 BP.  
K  
C ABK50102;  
K  
F 15-JUL-2002 (first entry)  
K  
E Allele specific hybridisation probe.  
K  
W Optimal reagent oligonucleotide; target nucleic acid evaluation;  
W target feature; exclusion value; ranking value; sequence window;  
W hybridisation; probe; ss.  
K  
S Synthetic.  
K  
N WO200229379-A2.  
K  
C 11-APR-2002.  
K  
F 04-OCT-2001; 2001WO-US031037.  
K  
R 04-OCT-2000; 2000US-0237383P.  
K  
A (CELA-) CELADON LAB INC.  
K  
I Peterson RJ;  
K  
R WPI; 2002-340129/37.  
K  
F Determining an optimal reagent oligonucleotide for evaluating a target  
F nucleic acid having a target feature, involves defining a set of  
F exclusion values and/or ranking values specific to a biochemical method.  
K  
S Example; Fig 2A; 91pp; English.  
K  
C The present invention relates to a new method for determining an optimal  
C reagent oligonucleotide for evaluating a target nucleic acid having a  
C target feature. The method comprises defining a set of exclusion values  
C and/or ranking values specific to the method, defining a sequence window  
C adjacent to the target, and generating candidate reagent oligonucleotides  
C complementary to the sense and/or antisense strands of the target within  
C the window. The method can be used for determining an optimal reagent  
C oligonucleotide sequence for use in a biochemical method for evaluating a  
C target nucleic acid sequence having a target feature. The present nucleic  
C acid sequence represent an allele specific hybridisation probe that was  
C used in the methods of the invention in numbering systems  
K  
2 Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15  
| | | | | | | | | | | | | | | |  
C 3 CATCGCCTGGACTCC 17

ESULT 8  
3K50102

ADT93449;  
13-JAN-2005 (first entry)  
Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.  
SNP detection; beta3 adrenaline receptor; ss; probe.  
Homo sapiens.  
Key Location/Qualifiers  
modified\_base 1  
/\*tag= a  
/mod\_base= OTHER  
/note= "OTHER = Linked to BODIPY FL group"  
modified\_base 20  
/\*tag= b  
/mod\_base= OTHER  
/note= "OTHER = Linked to P group"  
WO2004092385-A1.  
28-OCT-2004.  
16-APR-2004; 2004WO-JP005525.  
18-APR-2003; 2003JP-00114381.  
(ARKR-) ARKRAY INC.  
Hirai M;  
WPI; 2004-784610/77.  
Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
receptor gene having single nucleotide polymorphism, labeled at terminal  
with fluorescent dye and shows decrease in fluorescence of fluorescent  
dye upon hybridization.  
Claim 2; SEQ ID NO 9; 31pp; Japanese.  
The invention relates to a novel nucleic acid probe which is labelled at  
a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
of the fluorescent dye is observed upon hybridisation. The probe  
comprises a base sequence derived from a fully defined sequence of 1227  
nucleotides as given in the specification and being labelled at the 3' or  
5' end with a fluorescent dye. The probe of the invention may be useful  
for detecting a mutation or single nucleotide polymorphism (SNP) in the  
beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
contamination of the amplified product is prevented and the process is  
automated. The current sequence is that of the fluorescent-labelled probe  
(SEQ ID 5) of the invention which was targeted to human beta3 adrenaline  
receptor (B3AR) T190 variant DNA.  
Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 15; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CATCGCCTGGACTCC 15  
|||||||  
1 CATCGCCTGGACTCC 15



AAF96885;

18-NOV-2004 (revised)  
06-JUN-2001 (first entry)

Human gene single nucleotide polymorphism #1646.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.

Homo sapiens.  
Unidentified.

Key	Location/Qualifiers
variation	11
	/*tag= a
	/standard_name= "Single nucleotide polymorphism"

WO200118250-A2.

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.  
26-JUL-2000; 2000US-0220947P.  
16-AUG-2000; 2000US-0225724P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.  
(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;  
WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.

Example; Page 159; 242pp; English.

The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPs shown in the specification

Revised record issued on 18-NOV-2004 : The variation feature was incorrectly given a captial V

Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 CATCGCCTGGACTCC 15
  |||||
4 CATCGCCTGGACTCC 18

```

DO26525

ADO26525 standard; DNA; 25 BP.  
ADO26525;  
12-AUG-2004 (first entry)  
Novel hybridisation detection-related oligonucleotide SeqID1.  
hybridisation detection; immobilised probe; AC impedance;  
foetal genome analysis; ss.

Unidentified.  
WO2004044570-A1.  
27-MAY-2004.  
30-SEP-2003; 2003WO-JP012499.  
14-NOV-2002; 2002JP-00331059.  
(TOYA-) TOYAMA PREFECTURE.  
(COSE-) COSEL CO LTD.  
(TATE-) TATEYAMA KAGAKU IND CO LTD.  
(TOXX ) TOYO KAKO CO LTD.

Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;  
Nakagawa A, Mizuhara T, Mizushima M, Nakada M;  
WPI; 2004-420427/39.

Detection of hybridization of an immobilized probe to a target nucleic acid by measuring AC impedance across the carrier surface for specific gene detection in investigation and diagnosis of disease.

Example; SEQ ID NO 1; 33pp; Japanese.

This invention relates to a novel method of detecting hybridisation of an immobilised probe to a target nucleic acid using measurement of AC impedance. Detection of specific genes and gene sequences in nucleic acid samples (such as samples of genomic DNA) may be useful for diagnosis, prediction and prevention of genetic disorders and analysis of foetal genome. Hybridisation is detected with high accuracy and sensitivity without the use of dyes. The present sequence is that of an oligonucleotide which was used in the exemplification of the invention.

Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCC 15  
|||||||  
6 CATCGCCTGGACTCC 20

ESULT 11  
3L40567

ABL40567 standard; DNA; 26 BP.  
ABL40567;  
17-JUN-2002 (first entry)  
Primer #7 used in a base polymorphism detection method.  
Polymorphism; nucleic acid detection; endonuclease; probe; ADRB2;  
hybridisation; PCR primer; ss

Synthetic.  
 JP2002034598-A.  
 05-FEB-2002.  
 27-JUL-2000; 2000JP-00226912.  
 27-JUL-2000; 2000JP-00226912.  
 (TOYM ) TOYOBO KK.  
 WPI; 2002-298820/34.  
 Detection of base polymorphism.  
 Disclosure; Page 10; 10pp; Japanese.  
 The invention relates to a method for detecting base polymorphism. The method involves (1) amplifying the nucleic acid fragment containing base polymorphism of the specific nucleic acid sequence; (2) hybridising the amplified nucleic acid with at least two polymorphism-specific probes; (3) treating with RNA-selective cleavage endonuclease; (4) measuring detecting signals of each probe; and (5) identifying polymorphism by the ratio of each detecting signals. The probe can be used for detecting base polymorphism. The present sequence represents a PCR primer used in the course of the invention  
 Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 6; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCC 15  
 |||||  
 9 CATCGCCTGGACTCC 23

RESULT 12  
 DT93453  
 ADT93453 standard; DNA; 34 BP.  
 ADT93453;  
 13-JAN-2005 (first entry)  
 Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.  
 single nucleotide polymorphism; SNP; SNP detection;  
 beta3 adrenaline receptor; ds.  
 Homo sapiens.  
 Key Location/Qualifiers  
 variation replace(19,C)  
 /\*tag= a  
 /standard\_name= "Single nucleotide polymorphism"  
 WO2004092385-A1.  
 28-OCT-2004.  
 16-APR-2004; 2004WO-JP005525.  
 18-APR-2003; 2003JP-00114381.  
 (ARKR-) ARKRAY INC.  
 Hiroki M.

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Example 1; Fig 1; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment of the invention.

Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match: 100.0%; Score 15; DB 13; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 CATCGCCTGGACTCC 15
  |||||
12 CATCGCCTGGACTCC 26
```

ESULT 13

AC73164

AAC73164 standard; DNA; 21 BP.

AAC73164;

02-FEB-2001 (first entry)

SNP flanking sequence #24 used in multiplexing PCR/SBE assay.

Oligonucleotide array; genotyping; single base extension reaction; SBE; polymorphic locus; single nucleotide polymorphism; ss.

Unidentified.

WO200058516-A2.

05-OCT-2000.

27-MAR-2000; 2000WO-US008069.

26-MAR-1999; 99US-0126473P.

23-JUN-1999; 99US-0140359P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

(AFFY-) AFFYMETRIX INC.

Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ; Ryder T, Sklar P;

WPI; 2000-656171/63.

Universal array of oligonucleotides tags attached to a solid substrate along with locus-specific tagged oligonucleotides useful in genotyping using single base extension reactions.

Example 2; Page 50; 70pp; English

The present invention relates to an oligonucleotide array comprising oligonucleotide tags fixed to a solid substrate. The oligonucleotide array is useful for genotyping a nucleic acid sample at one or more loci via single base extension (SBE) reactions. A pair of primers is used to amplify a polymorphic locus in a sample e.g. a single nucleotide polymorphism (SNP). The present sequence is one such polymorphic locus used in the present invention. The amplified nucleic acid product is then used as a template in a SBE reaction with an extension primer. The SBE reaction products are used to form the oligonucleotide array. Note: This sequence includes a SNP represented by the degenerate codon in the sequence

Sequence 21 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 1 Other;

Query Match 100.0%; Score 15; DB 3; Length 21;  
Best Local Similarity 93.3%; Pred. No. 3.8e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCC 15  
|||||||:|||||||  
4 CATCGCCYGGACTCC 18

ESULT 14

AA04696

AAA04696 standard; DNA; 29 BP.

AAA04696;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene ADRB3.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999; 99EP-00250150.

07-MAY-1998; 98US-0084641P.

03-MAY-1999; 99US-00304232.

(AFFY-) AFFYMETRIX INC.

(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

Disclosure; Page 45; 53pp; English.

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension and in hypertension

hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 15; DB 3; Length 29;  
Best Local Similarity 93.3%; Pred. No. 3.9e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCC 15

[tart](#) | [next page](#)

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104105\_us-10-553-509-11.szlm60.rni.

[Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104105\_us-10-53-509-11.szlm60.rni.

[Start](#)

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 06:40:47 ; Search time 57.7079 Seconds  
(without alignments)  
518.781 Million cell updates/sec

Title: US-10-553-509-11  
Effect score: 16  
Sequence: 1 catcgctggactccg 16

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1475510

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
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10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	16	100.0	17	2	US-08-446-530-5	Sequence 5, Appli
2	16	100.0	17	2	US-08-446-530-7	Sequence 7, Appli
3	16	100.0	17	2	US-09-097-562-5	Sequence 5, Appli
4	16	100.0	17	2	US-09-097-562-7	Sequence 7, Appli
5	15.6	100.0	21	3	US-09-657-472-1650	Sequence 1650, Ap
6	15.6	100.0	22	3	US-09-657-472-1650	Sequence 1650, Ap

1--Start Fragment-->RES001 1

S-08-446-530-5/c

Sequence 5, Application US/08446530

Patent No. 5766851

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,530  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

S-08-446-530-5

Query Match 100.0%; Score 16; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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17 CATCGCCTGGACTCCG 2

RESULT 2

S-08-446-530-7

Sequence 7, Application US/08446530

Patent No. 5766851

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,530  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-446-530-7

Query Match 100.0%; Score 16; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||||  
1 CATCGCCTGGACTCCG 16

RESULT 3

3-09-097-562-5/c

Sequence 5, Application US/09097562

Patent No. 5877283

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS  
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,562  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,530  
FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO. 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-09-097-562-5

Query Match 100.0%; Score 16; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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o      17 CATCGCCTGGACTCCG 2
  
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RESULT 4

3-09-097-562-7

Sequence 7, Application US/09097562

Patent No. 5877283

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.

APPLICANT: Walston, Jeremy

APPLICANT: Silver, Kristi

TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE

TITLE OF INVENTION: II DIABETES MELLITUS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,562

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,530

FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-09-097-562-7

Query Match 100.0%; Score 16; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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o      1 CATCGCCTGGACTCCG 16
  
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# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104105\_us-10-553-509-12.szlm60.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104105\_us-10-53-509-12.szlm60.rni.

[Start](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 06:40:47 ; Search time 54.1011 Seconds  
(without alignments)  
518.781 Million cell updates/sec

Title: US-10-553-509-12  
Effect score: 15  
Sequence: 1 catcgctggactcc 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1475510

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	2	15	100.0	17	2	US-08-446-530-7	Sequence 7, Appli
2	3	15	100.0	17	2	US-09-097-562-5	Sequence 5, Appli
	4	15	100.0	17	2	US-09-097-562-7	Sequence 7, Appli
	5	14.6	100.0	21	3	US-09-657-472-1650	Sequence 1650, Ap
	6	14.6	100.0	22	3	US-09-657-472-1650	Sequence 1650, Ap

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9	13.4	89.3	17	2	US-09-097-562-6	Sequence 6, Appli
10	13.4	89.3	17	2	US-09-097-562-8	Sequence 8, Appli
11	13.4	89.3	33	2	US-08-646-367-19	Sequence 19, Appl
12	13.4	89.3	35	3	US-09-269-332-21	Sequence 21, Appl
13	13.4	89.3	39	2	US-08-478-039-44	Sequence 44, Appl
14	13.4	89.3	39	2	US-08-476-349A-44	Sequence 44, Appl
15	13.4	89.3	39	3	US-08-523-894-37	Sequence 37, Appl
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23	11.8	78.7	18	2	US-09-213-767-17	Sequence 17, Appl
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38	11.4	76.0	16	2	US-08-774-310-391	Sequence 391, App
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42	11.4	76.0	25	3	US-08-469-260A-655	Sequence 655, App
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45	11.4	76.0	25	3	US-08-488-446-698	Sequence 698, App

# ALIGNMENTS

## ESULT 1

3-08-446-530-5/c

Sequence 5, Application US/08446530

Patent No. 5766851

## GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.

APPLICANT: Walston, Jeremy

APPLICANT: Silver, Kristi

TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE

TITLE OF INVENTION: II DIABETES MELLITUS

NUMBER OF SEQUENCES: 28

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,530

FILING DATE: 19-MAY-1995

CLASSIFICATION: 425

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

3-08-446-530-5

Query Match 100.0%; Score 15; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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y      1 CATCGCCTGGACTCC 15
      |||||
o      17 CATCGCCTGGACTCC 3
  
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RESULT 2

3-08-446-530-7

Sequence 7, Application US/08446530  
Patent No. 5766851

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,530  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

3-08-446-530-7

Query Match 100.0%; Score 15; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15  
|||||  
O 1 CATCGCCTGGACTCC 15

ESULT 3  
3-09-097-562-5/c  
Sequence 5, Application US/09097562  
Patent No. 5877283

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,562  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,530  
FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-09-097-562-5

Query Match 100.0%; Score 15; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15  
|||||  
O 17 CATCGCCTGGACTCC 3

ESULT 4  
3-09-097-562-7  
Sequence 7, Application US/09097562  
Patent No. 5877283

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,562  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,530  
FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

S-09-097-562-7

Query Match 100.0%; Score 15; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||  
O 1 CATCGCCTGGACTCC 15

RESULT 5

S-09-657-472-1650

Sequence 1650, Application US/09657472

Patent No. 6727063

GENERAL INFORMATION:

APPLICANT: Lander, Eric S.  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Bolk, Stacey  
APPLICANT: Daley, George Q.  
APPLICANT: McCarthy, Jeanette J.

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

FILE REFERENCE: 2825.1027-001

CURRENT APPLICATION NUMBER: US/09/657,472

CURRENT FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/153,357

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US 60/220,947

PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: US 60/225,724

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2551

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1650

LENGTH: 21

TYPE: DNA



3-09-657-472-1650

Query Match 100.0%; Score 15; DB 3; Length 21;  
Best Local Similarity 93.3%; Pred. No. 92;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCC 15  
||| ||| : ||| |||  
o 4 CATGCCYGGACTCC 18

ESULT 6

3-09-304-232-896

Sequence 896, Application US/09304232

Patent No. 6525185

GENERAL INFORMATION:

APPLICANT: Fan, Jian Bing

APPLICANT: Chakravarti, Aravinda

APPLICANT: Halushka, Marc Kenneth

APPLICANT: Case Western Reserve University School of Medicine

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Polymorphisms Associated With

TITLE OF INVENTION: Hypertension

FILE REFERENCE: 018547-034210US

CURRENT APPLICATION NUMBER: US/09/304,232

CURRENT FILING DATE: 1999-05-03

EARLIER APPLICATION NUMBER: US 60/084,641

EARLIER FILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 909

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 896

LENGTH: 29

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: ADRB3EX1 416

3-09-304-232-896

Query Match 100.0%; Score 15; DB 3; Length 29;  
Best Local Similarity 93.3%; Pred. No. 94;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCC 15  
||| ||| : ||| |||  
o 8 CATGCCYGGACTCC 22

ESULT 7

3-08-446-530-6/c

Sequence 6, Application US/08446530

Patent No. 5766851

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.

APPLICANT: Walston, Jeremy

APPLICANT: Silver, Kristi

TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE

TITLE OF INVENTION: II DIABETES MELLITUS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0 Version #1.20

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104100\_us-10-553-509- 8.szlm60.rng.

[Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104100\_us-10-53-509-8.szlm60.rng.

[Start](#) | [next page](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

Method: nucleic - nucleic search, using sw model

Run on: December 15, 2006, 05:57:43 ; Search time 241.124 Seconds  
(without alignments)  
578.313 Million cell updates/sec

Title: US-10-553-509-8  
Effect score: 20  
Sequence: 1 cgtggccatcgccccggactc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searches: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5397982

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8.szlm60.rng  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	20	100.0	20	12	1980140	1980140	

3	20	100.0	34	13	ADT93454	Adt93454 Human bet
4	20	100.0	41	6	ABK50104	Abk50104 Sense str
5	19.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
6	19.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
7	19	95.0	25	4	AAC89164	Aac89164 Sample DN
8	19	95.0	25	12	ADO26526	Ado26526 Novel hyb
9	18.4	92.0	34	13	ADT93453	Adt93453 Human bet
10	18	90.0	20	14	AEC91759	Aec91759 Probe 5T-
11	17.4	87.0	25	12	ADO26525	Ado26525 Novel hyb
12	17	85.0	21	14	AEC91760	Aec91760 Probe 3T-
13	17	85.0	27	3	AAA73177	Aaa73177 Beta-3-ad
14	16.6	83.0	21	3	AAC73164	Aac73164 SNP flank
15	16.4	82.0	25	6	ABL40568	Abl40568 Primer #8
16	16.4	82.0	26	6	ABL40567	Abl40567 Primer #7
17	15.4	77.0	21	4	AAF96885	Aaf96885 Human gen
18	15.4	77.0	27	3	AAA73176	Aaa73176 Beta-3-ad
19	15	75.0	16	13	ADT93445	Adt93445 Fluoresce
20	15	75.0	19	13	ADT93446	Adt93446 Fluoresce
21	14.8	74.0	20	4	AAF31792	Aaf31792 Human RAN
22	14.4	72.0	19	6	ABK50102	Abk50102 Allele sp
23	14.2	71.0	60	6	ABN47900	Abn47900 Human spl
24	14	70.0	17	2	AAT58988	Aat58988 Obesity a
25	14	70.0	17	2	AAT58990	Aat58990 Obesity a
26	14	70.0	17	15	AEE87557	Aee87557 Human min
27	14	70.0	19	13	ADT93447	Adt93447 Fluoresce
28	14	70.0	20	14	AED47650	Aed47650 Human bet
29	14	70.0	25	13	ADR55076	Adr55076 Drug ther
30	14	70.0	41	2	AAV13420	Aav13420 R64 allele
31	14	70.0	41	3	AAA73179	Aaa73179 Beta-3-ad
32	13.8	69.0	42	7	ADI92927	Adi92927 Thermus s
33	13.6	68.0	20	12	ADM15299	Adm15299 Human mPG
34	13.6	68.0	36	12	ADL24391	Adl24391 Multiple
35	13.6	68.0	36	12	ADL24405	Adl24405 Multiple
36	13.6	68.0	51	4	AAI79557	Aai79557 Human sil
37	13.6	68.0	54	6	AAD37446	Aad37446 Human nec
38	13.4	67.0	15	6	ABK50103	Abk50103 Oligonucl
39	13.4	67.0	20	10	ADC51219	Adc51219 Oligonucl
40	13.4	67.0	20	10	ADF55593	Adf55593 Oligonucl
41	13.4	67.0	20	12	ADQ67903	Adq67903 Beta-3-ad
42	13.4	67.0	30	4	AAF44557	Aaf44557 Mouse DSS
43	13.4	67.0	32	15	AEF10675	Aef10675 Aspergill
44	13.4	67.0	48	4	AAH97483	Aah97483 Human Chk
45	13.4	67.0	48	5	ADV61702	Adv61702 HBV amber

ALIGNMENTS

```

ESULT 1
DT93448
D  ADT93448 standard; DNA; 20 BP.
K
C  ADT93448;
K
F  13-JAN-2005  (first entry)
K
E  Fluorescent probe targeted to human B3AR C190 variant DNA - SEQ ID 8.
K
W  SNP detection; beta3 adrenaline receptor; ss; probe.
K
S  Homo sapiens.
K
H  Key          Location/Qualifiers
F  modified_base 20
F                      /*tag= a
F                      /mod_base= OTHER
F                      /note= "OTHER = Linked to TAMRA group"
K
N  WO2004092385-A1.
v

```

16-APR-2004; 2004WO-JP005525.  
18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 2; SEQ ID NO 8; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the fluorescent-labelled probe (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline receptor (B3AR) C190 variant DNA.

Sequence 20 BP; 2 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTGGCCATCGCCCGGACTC 20  
|||||||  
1 CGTGGCCATCGCCCGGACTC 20

RESULT 2  
EC91741

AEC91741 standard; DNA; 20 BP.

AEC91741;

01-DEC-2005 (first entry)

Primer 3CB-B3AR-mt-F2-20 SEQ ID NO:17.

DNA detection; SNP detection; primer; ss.

Synthetic.

JP2005261354-A.

29-SEP-2005.

19-MAR-2004; 2004JP-00080974.

19-MAR-2004; 2004JP-00080974.

(KYOT-) KYOTO DAIICHI KAGAKU KK.

Inose K;

WPI. 2005 662120/60

Detecting target nucleic acid, involves detecting target based on change of fluorescence intensity due to formation or dissociation of hybrid of target nucleic acid and hybridization probe having 5-carboxy fluorescein.

Example 6; SEQ ID NO 17; 28pp; Japanese.

The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxyl]aceto hydrazide (Cascade blue). Also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a primer used in an example from the present invention.

Sequence 20 BP; 2 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 20;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTGGCCATCGCCCGGACTC 20

|||||||

1 CGTGGCCATCGCCCGGACTC 20

ESULT 3

DT93454

ADT93454 standard; DNA; 34 BP.

ADT93454;

13-JAN-2005 (first entry)

Human beta3 adrenaline receptor (B3AR) C190 variant DNA fragment.

single nucleotide polymorphism; SNP; SNP detection;  
beta3 adrenaline receptor; ds.

Homo sapiens.

Key Location/Qualifiers  
variation replace(19,T)  
/\*tag= a  
/standard\_name= "Single nucleotide polymorphism"

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

10 APR 2002. 2002 JP 00114281

A (ARKR-) ARKRAY INC.  
K  
I Hirai M;  
K  
R WPI; 2004-784610/77.  
K  
T Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
T receptor gene having single nucleotide polymorphism, labeled at terminal  
T with fluorescent dye and shows decrease in fluorescence of fluorescent  
T dye upon hybridization.  
K  
S Example 1; Fig 1; 31pp; Japanese.  
K  
C The invention relates to a novel nucleic acid probe which is labelled at  
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
C of the fluorescent dye is observed upon hybridisation. The probe  
C comprises a base sequence derived from a fully defined sequence of 1227  
C nucleotides as given in the specification and being labelled at the 3' or  
C 5' end with a fluorescent dye. The probe of the invention may be useful  
C for detecting a mutation or single nucleotide polymorphism (SNP) in the  
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
C contamination of the amplified product is prevented and the process is  
C automated. The current sequence is that of the human beta3 adrenaline  
C receptor (B3AR) C190 variant DNA fragment of the invention.  
K  
Q Sequence 34 BP; 5 A; 14 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 34;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGTGGCCATCGCCCGGACTC 20  
|||  
C 6 CGTGGCCATCGCCCGGACTC 25

ESULT 4  
BK50104  
D ABK50104 standard; DNA; 41 BP.  
K  
C ABK50104;  
K  
T 15-JUL-2002 (first entry)  
K  
E Sense strand of target nucleic acid.  
K  
W Optimal reagent oligonucleotide; target nucleic acid evaluation;  
W target feature; exclusion value; ranking value; sequence window;  
W single nucleotide polymorphism; SNP; ds.  
K  
S Synthetic.  
K  
H Key Location/Qualifiers  
T variation replace(21,T)  
T /\*tag= a  
T /standard\_name= "Single nucleotide polymorphism"  
K  
N WO200229379-A2.  
K  
D 11-APR-2002.  
K  
F 04-OCT-2001; 2001WO-US031037.  
K  
R 04-OCT-2000; 2000US-0237383P.  
K  
A (CELA-) CELADON LAB INC.  
K  
I Peterson RJ;  
v

Determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature, involves defining a set of exclusion values and/or ranking values specific to a biochemical method.  
 Example; Fig 4A; 91pp; English.  
 The present invention relates to a new method for determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature. The method comprises defining a set of exclusion values and/or ranking values specific to the method, defining a sequence window adjacent to the target, and generating candidate reagent oligonucleotides complementary to the sense and/or antisense strands of the target within the window. The method can be used for determining an optimal reagent oligonucleotide sequence for use in a biochemical method for evaluating a target nucleic acid sequence having a target feature. The present nucleic acid sequence represent the sense strand of a target nucleic acid. This sequence was used in the methods of the invention in a sequence window  
 Sequence 41 BP; 7 A; 16 C; 11 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CGTGGCCATCGCCCGGACTC 20.  
 |||||  
 8 CGTGGCCATCGCCCGGACTC 27

RESULT 5  
 AA04696  
 AAA04696 standard; DNA; 29 BP.  
 AAA04696;  
 22-MAY-2000 (first entry)  
 Polymorphic fragment of hypertension associated gene ADRB3.  
 Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.  
 Homo sapiens.  
 EP955382-A2.  
 10-NOV-1999.  
 07-MAY-1999; 99EP-00250150.  
 07-MAY-1998; 98US-0084641P.  
 03-MAY-1999; 99US-00304232.  
 (AFFY-) AFFYMETRIX INC.  
 (UYCA-) UNIV CASE WESTERN RESERVE.  
 Fan JB, Chakravarti A, Haluska MK;  
 WPI; 2000-107928/10.  
 Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.  
 Disclosure: Page 45; 52pp; English

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 3; Length 29;  
 Best Local Similarity 95.0%; Pred. No. 21;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

1 CGTGGCCATCGCCCGGACTC 20
  |||||:|||||
2 CGTGGCCATCGCCYGGACTC 21
  
```

#### ESULT 6

3K50101

ABK50101 standard; DNA; 41 BP.

ABK50101;

15-JUL-2002 (first entry)

Nucleic acid sequence used for sequence formatting.

Optimal reagent oligonucleotide; target nucleic acid evaluation;  
 target feature; exclusion value; ranking value; sequence window;  
 sequence formatting; ds.

Synthetic.

WO200229379-A2.

11-APR-2002.

04-OCT-2001; 2001WO-US031037.

04-OCT-2000; 2000US-0237383P.

(CELA-) CELADON LAB INC.

Peterson RJ;

WPI; 2002-340129/37.

Determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature, involves defining a set of exclusion values and/or ranking values specific to a biochemical method.

Example; Fig 1B; 91pp; English.

The present invention relates to a new method for determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature. The method comprises defining a set of exclusion values



and/or flanking values specific to the method, defining a sequence window adjacent to the target, and generating candidate reagent oligonucleotides complementary to the sense and/or antisense strands of the target within the window. The method can be used for determining an optimal reagent oligonucleotide sequence for use in a biochemical method for evaluating a target nucleic acid sequence having a target feature. The present nucleic acid sequence represent a DNA molecule used in the methods of the invention for nucleic acid sequence formatting

Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 6; Length 41;  
Best Local Similarity 95.0%; Pred. No. 20;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CGTGGCCATCGCCCGGACTC 20  
|||||||:|||||  
8 CGTGGCCATCGCCYGGACTC 27

ESULT 7  
AC89164/c  
AAC89164 standard; DNA; 25 BP.  
AAC89164;  
08-MAR-2001 (first entry)  
Sample DNA #2 used in a method for gene analysis.  
Gene analysis; infectious disease; genetic disease; gene expression; ss.  
Unidentified.

Key	Location/Qualifiers
modified_base	1
	/*tag= a
	/mod_base= OTHER
	/note= "OTHER = CY5 labelled A"

EP1055735-A2.  
29-NOV-2000.  
25-MAY-2000; 2000EP-00110932.  
25-MAY-1999; 99JP-00144749.  
(MITU ) MITSUBISHI CHEM CORP.  
Hatakeyama K;  
WPI; 2001-042414/06.

A method for gene analysis, e.g. for gene diagnosis of infectious or genetic diseases, by detecting hybridization between a nucleic acid probe and sample in the presence of a double-stranded DNA-binding protein.

Example 2; Page 10; 18pp; English.

The present invention relates to a method for gene analysis. The method comprises detecting hybridisation, which is caused in the presence of a double-stranded DNA-binding protein, between a probe nucleic acid and a sample nucleic acid. The method is useful for gene analysis, particularly in determining the nucleotide sequence of nucleic acids, in gene diagnosis of infectious or genetic diseases, or monitoring of genome DNA expression. The present sequence is a sample DNA used in the method of the present invention

Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 GTGGCCATCGCCCGGACTC 20  
|||||||  
25 GTGGCCATCGCCCGGACTC 7

ESULT 8  
DO26526

ADO26526 standard; DNA; 25 BP.  
ADO26526;  
12-AUG-2004 (first entry)  
Novel hybridisation detection-related oligonucleotide SeqID2.  
hybridisation detection; immobilised probe; AC impedance;  
foetal genome analysis; ss.  
Unidentified.  
WO2004044570-A1.  
27-MAY-2004.  
30-SEP-2003; 2003WO-JP012499.  
14-NOV-2002; 2002JP-00331059.  
(TOYA-) TOYAMA PREFECTURE.  
(COSE-) COSEL CO LTD.  
(TATE-) TATEYAMA KAGAKU IND CO LTD.  
(TOXX ) TOYO KAKO CO LTD.

Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;  
Nakagawa A, Mizuhara T, Mizushima M, Nakada M;  
WPI; 2004-420427/39.

Detection of hybridization of an immobilized probe to a target nucleic acid by measuring AC impedance across the carrier surface for specific gene detection in investigation and diagnosis of disease.

Example; SEQ ID NO 2; 33pp; Japanese.

This invention relates to a novel method of detecting hybridisation of an immobilised probe to a target nucleic acid using measurement of AC impedance. Detection of specific genes and gene sequences in nucleic acid samples (such as samples of genomic DNA) may be useful for diagnosis, prediction and prevention of genetic disorders and analysis of foetal genome. Hybridisation is detected with high accuracy and sensitivity without the use of dyes. The present sequence is that of an oligonucleotide which was used in the exemplification of the invention.

Sequence 25 BP; 4 A; 10 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 GTGGCCATCGCCCGGACTC 20  
|||||||  
1 GTGGCCATCGCCCGGACTC 19

ESULT 9  
DT93453

ADO26526 standard; DNA; 25 BP.

ADT93453;

13-JAN-2005 (first entry)

Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.

single nucleotide polymorphism; SNP; SNP detection;  
beta3 adrenaline receptor; ds.

Homo sapiens.

Key Location/Qualifiers  
variation replace(19,C)  
/\*tag= a  
/standard\_name= "Single nucleotide polymorphism"

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
receptor gene having single nucleotide polymorphism, labeled at terminal  
with fluorescent dye and shows decrease in fluorescence of fluorescent  
dye upon hybridization.

Example 1; Fig 1; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at  
a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
of the fluorescent dye is observed upon hybridisation. The probe  
comprises a base sequence derived from a fully defined sequence of 1227  
nucleotides as given in the specification and being labelled at the 3' or  
5' end with a fluorescent dye. The probe of the invention may be useful  
for detecting a mutation or single nucleotide polymorphism (SNP) in the  
beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
contamination of the amplified product is prevented and the process is  
automated. The current sequence is that of the human beta3 adrenaline  
receptor (B3AR) T190 variant DNA fragment of the invention.

Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 13; Length 34;  
Best Local Similarity 95.0%; Pred. No. 74;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

1 CGTGGCCATCGCCCGGACTC 20
  |||||
6 CGTGGCCATCGCCTGGACTC 25

```

ESULT 10

EC91759

AEC91759 standard; DNA; 20 BP.

AEC91759;

01-DEC-2005 (first entry)

Probe 5T B3AR m TMS F1 20 SEQ ID NO.25

DNA detection; SNP detection; probe; ss.  
 Synthetic.  
 JP2005261354-A.  
 29-SEP-2005.  
 19-MAR-2004; 2004JP-00080974.  
 19-MAR-2004; 2004JP-00080974.  
 (KYOT-) KYOTO DAIICHI KAGAKU KK.  
 Inose K;  
 WPI; 2005-662138/68.  
 Detecting target nucleic acid, involves detecting target based on change of fluorescence intensity due to formation or dissociation of hybrid of target nucleic acid and hybridization probe having 5-carboxy fluorescein.  
 Example 10; SEQ ID NO 35; 28pp; Japanese.  
 The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto hydrazide (Cascade blue). Also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a probe used in an example from the present invention.

Sequence 20 BP; 2 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTGGCCATCGCCCGGAC 18  
 |||||  
 3 CGTGGCCATCGCCCGGAC 20

ESULT 11  
 J026525  
 ADO26525 standard; DNA; 25 BP.  
 ADO26525;  
 12-AUG-2004 (first entry)  
 Novel hybridization detection related oligonucleotide SeqID1

W hybridisation detection; immobilised probe; AC impedance;  
W foetal genome analysis; ss.  
K  
S Unidentified.  
K  
N WO2004044570-A1.  
K  
D 27-MAY-2004.  
K  
F 30-SEP-2003; 2003WO-JP012499.  
K  
R 14-NOV-2002; 2002JP-00331059.  
K  
A (TOYA-) TOYAMA PREFECTURE.  
A (COSE-) COSEL CO LTD.  
A (TATE-) TATEYAMA KAGAKU IND CO LTD.  
A (TOXX ) TOYO KAKO CO LTD.  
K  
I Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;  
I Nakagawa A, Mizuhara T, Mizushima M, Nakada M;  
K  
R WPI; 2004-420427/39.  
K  
T Detection of hybridization of an immobilized probe to a target nucleic  
T acid by measuring AC impedance across the carrier surface for specific  
T gene detection in investigation and diagnosis of disease.  
K  
S Example; SEQ ID NO 1; 33pp; Japanese.  
K  
C This invention relates to a novel method of detecting hybridisation of an  
C immobilised probe to a target nucleic acid using measurement of AC  
C impedance. Detection of specific genes and gene sequences in nucleic acid  
C samples (such as samples of genomic DNA) may be useful for diagnosis,  
C prediction and prevention of genetic disorders and analysis of foetal  
C genome. Hybridisation is detected with high accuracy and sensitivity  
C without the use of dyes. The present sequence is that of an  
C oligonucleotide which was used in the exemplification of the invention.  
K  
Q Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 12; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 2 GTGGCCATCGCCCGGACTC 20  
| | | | | | | | | | | | | | | |  
O 1 GTGGCCATCGCCTGGACTC 19

ESULT 12  
EC91760  
D AEC91760 standard; DNA; 21 BP.  
K  
C AEC91760;  
K  
T 01-DEC-2005 (first entry)  
K  
E Probe 3T-B3AR-w-IMS-F2-21 SEQ ID NO:36.  
K  
W DNA detection; SNP detection; probe; ss.  
K  
S Synthetic.  
K  
N JP2005261354-A.  
K  
D 29-SEP-2005.  
K  
F 19-MAR-2004; 2004JP-00080974.  
K  
D 19 MAR 2004; 2004JP 00080974

(KYOT-) KYOTO DAIICHI KAGAKU KK.  
Inose K;  
WPI; 2005-662138/68.  
Detecting target nucleic acid, involves detecting target based on change of fluorescence intensity due to formation or dissociation of hybrid of target nucleic acid and hybridization probe having 5-carboxy fluorescein.  
Example 10; SEQ ID NO 36; 28pp; Japanese.  
The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto hydrazide (Cascade blue). Also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a probe used in an example from the present invention.  
Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 14; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 GGCCATCGCCCGGACTC 20  
|||||||  
1 GGCCATCGCCCGGACTC 17

ESULT 13  
AA73177  
AAA73177 standard; DNA; 27 BP.  
AAA73177;  
28-NOV-2000 (first entry)  
Beta-3-adrenergic receptor R64 allele oligonucleotide SEQ ID NO:39.  
Amplification; target; hairpin; primer; blocking oligonucleotide; donor; acceptor; detection; telomerase activity; triamplification; PCR; allele-specific PCR; nucleic acid sequence-based amplification; strand displacement amplification; telomeric repeat amplification; cascade rolling circle amplification; in situ amplification; amplification refractory mutation system; ss.  
Unidentified.  
US6090552-A.

10 JUL 2000.  
X  
F 11-JUL-1997; 97US-00891516.  
X  
R 16-JUL-1996; 96US-00683667.  
R 03-JAN-1997; 97US-00778487.  
R 11-APR-1997; 97US-00837034.  
X

A (INTE-) INTERGEN CO.

X  
I Hohman RJ, Winn-Deen ES, Bhatnagar SK, Nazarenko IA;  
X  
R WPI; 2000-505149/45.  
X

T Use of labeled hairpin amplification oligonucleotides to detect  
T telomerase activity and to determine the presence of target nucleic acid  
T sequence in a sample.  
X

S Example 10; Col 56; 98pp; English.  
X

C The present invention describes the use of labelled hairpin amplification  
C oligonucleotides to detect telomerase activity and to determine the  
C presence of target nucleic acid sequence in a sample. The method can be  
C used to detect telomerase activity and to determine the presence of  
C target nucleic acid sequences in a sample and for detecting amplification  
C products of polymerase chain reaction, allele-specific polymerase chain  
C reaction, triamplification, nucleic acid sequence-based amplification,  
C strand displacement amplification, telomeric repeat amplification,  
C cascade rolling circle amplification, amplification refractory mutation  
C system or in situ amplification. The use of a universal hairpin primer  
C permits a closed tube format. Amplification and detection are performed  
C in the same tube so that no carry-over contamination with amplicon occurs  
C and consequently no false positive results are obtained. The present  
C sequence represents an oligonucleotide which is used in the  
C exemplification of the present invention  
X

2 Sequence 27 BP; 3 A; 9 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGTGGCCATCGCCCGGA 17  
|||  
O 11 CGTGGCCATCGCCCGGA 27

ESULT 14  
AC73164  
O AAC73164 standard; DNA; 21 BP.  
X

C AAC73164;  
X

T 02-FEB-2001 (first entry)  
X

E SNP flanking sequence #24 used in multiplexing PCR/SBE assay.  
X

N Oligonucleotide array; genotyping; single base extension reaction; SBE;  
N polymorphic locus; single nucleotide polymorphism; ss.  
X

S Unidentified.  
X

N WO200058516-A2.  
X

O 05-OCT-2000.  
X

F 27-MAR-2000; 2000WO-US008069.  
X

R 26-MAR-1999; 99US-0126473P.  
R 23-JUN-1999; 99US-0140359P.  
v

A (AFFY-) AFFYMETRIX INC.  
K  
I Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;  
I • Ryder T, Sklar P;  
K  
R WPI; 2000-656171/63.  
K  
F Universal array of oligonucleotides tags attached to a solid substrate  
F along with locus-specific tagged oligonucleotides useful in genotyping  
F using single base extension reactions.  
K  
S Example 7; Page 50; 70pp; English.  
K  
C The present invention relates to an oligonucleotide array comprising  
C oligonucleotide tags fixed to a solid substrate. The oligonucleotide  
C array is useful for genotyping a nucleic acid sample at one or more loci  
C via single base extension (SBE) reactions. A pair of primers is used to  
C amplify a polymorphic locus in a sample e.g. a single nucleotide  
C polymorphism (SNP). The present sequence is one such polymorphic locus  
C used in the present invention. The amplified nucleic acid product is then

[tart](#) | [next page](#)



# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104357\_us-10-553-509- 2\_copy\_165\_200.rng.

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This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104357\_us-10-553-509-2\_copy\_165\_200.rng.

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GenCore version 5.1.9  
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4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 14:32:10 ; Search time 177.031 Seconds  
(without alignments)  
1417.837 Million cell updates/sec

Title: US-10-553-509-2\_COPY\_165\_200  
Perfect score: 36  
Sequence: 1 cctgctggtcatcgtggccatcgcccggactccgag 36

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%				
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	36	100	0	100	14	20061214_104357_us-10-553-509-2_copy_165_200.rng

2	36	100.0	210	2	AAQ11762	Aax11762 Human bia
3	36	100.0	1227	13	ADT93442	Adt93442 Human bet
4	35.6	100.0	210	2	AAQ11762	Aax11762 Human bia
5	35.6	100.0	420	14	AEC91757	Aec91757 Template
6	35.6	100.0	2040	6	ABK11513	Abk11513 Human bet
7	35.6	100.0	5669	14	ADZ42281	Adz42281 Human bet
8	35.6	100.0	10306	6	ABK11451	Abk11451 Human bet
9	34.4	95.6	1003	12	ACH91802	Ach91802 Human gen
10	34.4	95.6	1185	6	ABX13060	Abx13060 Human bet
11	34.4	95.6	1185	14	AEA13746	Aea13746 Human bet
12	34.4	95.6	1227	2	AAQ55693	Aaq55693 DNA encod
13	34.4	95.6	1227	13	ADT93441	Adt93441 Human bet
14	34.4	95.6	1270	10	ACA56586	Aca56586 Human sig
15	34.4	95.6	1270	12	ADI56382	Adi56382 Human pol
16	34.4	95.6	2022	2	AAQ05731	Aaq05731 Beta 3 ad
17	34.4	95.6	2518	2	AAV23500	Aav23500 Human adr
18	34.4	95.6	2644	8	ABZ42630	Abz42630 Human bet
19	34.4	95.6	2644	11	ADN39372	Adn39372 Cancer/an
20	34.4	95.6	2644	12	ADO29809	Ado29809 Human GPC
21	34.4	95.6	2644	13	ADU50894	Adu50894 Human bet
22	34.4	95.6	2644	14	AEC83014	Aec83014 Breast ca
23	34.4	95.6	2644	14	AEE01346	Aee01346 Human G p
24	34.4	95.6	3682	2	AAQ65476	Aaq65476 Human bet
25	34.4	95.6	5669	13	ADU50893	Adu50893 Human bet
26	32.8	91.1	2000	2	AAQ74367	Aaq74367 Bovine be
27	31.2	86.7	75	10	ADD32084	Add32084 Human bet
28	31.2	86.7	2649	2	AAV30469	Aav30469 Canine be
29	31	86.1	41	6	ABK50104	Abk50104 Sense str
30	30.8	85.6	75	10	ADD32073	Add32073 Human bet
31	30.6	85.0	41	6	ABK50101	Abk50101 Nucleic a
32	29.6	82.2	75	10	ADD32083	Add32083 Human bet
33	29	80.6	34	13	ADT93454	Adt93454 Human bet
34	28	77.8	1203	12	ADO30100	Ado30100 Mouse GPC
35	28	77.8	1920	2	AAQ26808	Aaq26808 Murine ad
36	28	77.8	3437	2	AAQ65477	Aaq65477 Murine be
37	28	77.8	4749	3	AAZ98401	Aaz98401 Sheep bet
38	28	77.8	4749	6	ABK40733	Abk40733 Sheep bet
39	27.4	76.1	34	13	ADT93453	Adt93453 Human bet
40	27.4	76.1	330	2	AAV23501	Aav23501 3T3 deriv
41	27	75.0	27	3	AAA73177	Aaa73177 Beta-3-ad
42	26.4	73.3	1401	12	ADO30098	Ado30098 Mouse GPC
43	26.4	73.3	1525	3	AAZ98405	Aaz98405 Mouse bet
44	26.4	73.3	1525	6	ABK40737	Abk40737 Mouse bet
45	26.4	73.3	4401	3	AAZ98404	Aaz98404 Rhesus mo

# ALIGNMENTS

RESULT 1  
 EC91742/c  
 D AEC91742 standard; DNA; 100 BP.  
 K  
 C AEC91742;  
 K  
 T 01-DEC-2005 (first entry)  
 K  
 E Template B3AR-mt-R(141-240) SEQ ID NO:18.  
 K  
 W DNA detection; SNP detection; template; ds.  
 K  
 S Synthetic.  
 K  
 N JP2005261354-A.  
 K  
 D 29-SEP-2005.  
 K  
 F 19-MAR-2004; 2004JP-00080974.  
 K  
 R 19-MAR-2004; 2004JP-00080974.  
 V

Inose K;  
WPI; 2005-662138/68.

Detecting target nucleic acid, involves detecting target based on change of fluorescence intensity due to formation or dissociation of hybrid of target nucleic acid and hybridization probe having 5-carboxy fluorescein.

Example 6; SEQ ID NO 18; 28pp; Japanese.

The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxyl]aceto hydrazide (Cascade blue). Also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a template sequence used in an example from the present invention.

Sequence 100 BP; 19 A; 31 C; 34 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 36; DB 14; Length 100;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||||  
76 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 41

RESULT 2  
AX12815

AAX12815 standard; DNA; 210 BP.  
AAX12815;  
30-MAR-1999 (first entry)  
Human biallelic polymorphic DNA fragment ESTD-B3AR.  
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.  
Homo sapiens.  
WO9820165-A2.  
14-MAY-1998.  
05 NOV 1997. 0740 US020212

R 06-NOV-1996; 96US-0030455P.  
K  
A (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
K  
I .Lander ES, Wang D, Hudson T;  
K  
R WPI; 1998-286974/25.  
K  
I New isolated nucleic acid segments from the human genome - used for  
I determining polymorphic forms for use in e.g. forensics, paternity  
I testing or phenotypic typing for disease.  
K  
S Claim 1; Page 292; 310pp; English.  
K  
C AAX10269-X12937 are human DNA fragments which contain biallelic  
C polymorphic markers which have been isolated using the primers  
C represented in AAX09121-X10268. The base occupying the polymorphic site  
C is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments  
C can be used in methods for determining polymorphic forms in an individual  
C for use in e.g. forensics, paternity testing or for phenotypic typing for  
C diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan  
C syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,  
C familial hypercholesterolemia, polycystic kidney disease, hereditary  
C spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary  
C haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos  
C syndrome, osteogenesis imperfecta, acute intermittent porphyria,  
C autoimmune diseases, inflammation, cancer, diseases of the nervous  
C system, infection by pathogenic microorganisms, and characteristics such  
C as longevity, appearance (e.g. baldness, obesity), strength, speed,  
C endurance, fertility, and susceptibility or receptivity to particular  
C drugs or therapeutic treatments. The isolated polymorphic nucleic acid  
C segments can also be used to produce medicaments for the treatment or  
C prophylaxis of such diseases  
K  
Q Sequence 210 BP; 24 A; 71 C; 79 G; 36 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 36; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCTGCTGGTTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||  
O 80 CCTGCTGGTTCATCGTGGCCATCGCCCGGACTCCGAG 115

ESULT 3  
DT93442  
O ADT93442 standard; DNA; 1227 BP.  
K  
C ADT93442;  
K  
I 13-JAN-2005 (first entry)  
K  
E Human beta3 adrenaline receptor (B3AR) C190 variant DNA.  
K  
W single nucleotide polymorphism; SNP; SNP detection;  
W beta3 adrenaline receptor; ds.  
K  
S Homo sapiens.  
K  
H Key Location/Qualifiers  
I variation replace(190,T)  
I /\*tag= a  
I /standard\_name= "Single nucleotide polymorphism"  
K  
N WO2004092385-A1.  
K  
O 28-OCT-2004.  
K  
O 16 APR 2004. 2004WO 0005525

18-APR-2003; 2003JP-00114381.  
(ARKR-) ARKRAY INC.  
Hirai M;  
WPI; 2004-784610/77.  
Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.  
Claim 1; SEQ ID NO 2; 31pp; Japanese.  
The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the human beta3 adrenaline receptor (B3AR) C190 variant DNA of the invention.  
Sequence 1227 BP; 125 A; 464 C; 391 G; 247 T; 0 U; 0 Other;

Query Match 100.0%; Score 36; DB 13; Length 1227;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||||  
165 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 200

ESULT 4  
AX11762  
AAX11762 standard; DNA; 210 BP.  
AAX11762;  
30-MAR-1999 (first entry)  
Human biallelic polymorphic DNA fragment ESTD-B3AR.  
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.  
Homo sapiens.  
WO9820165-A2.  
14-MAY-1998.  
05-NOV-1997; 97WO-US020313.  
06-NOV-1996; 96US-0030455P.  
(WHED ) WHITEHEAD INST BIOMEDICAL RES.  
Lander ES, Wang D, Hudson T;  
WPI; 1998-286974/25.

1 new isolated nucleic acid segments from the human genome used for  
P determining polymorphic forms for use in e.g. forensics, paternity  
P testing or phenotypic typing for disease.  
K  
3 Claim 1; Page 191; 310pp; English.  
K  
2 AAX10269-X12937 are human DNA fragments which contain biallelic  
2 polymorphic markers which have been isolated using the primers  
2 represented in AAX09121-X10268. The base occupying the polymorphic site  
2 is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments  
2 can be used in methods for determining polymorphic forms in an individual  
2 for use in e.g. forensics, paternity testing or for phenotypic typing for  
2 diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan  
2 syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,  
2 familial hypercholesterolemia, polycystic kidney disease, hereditary  
2 spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary  
2 haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos  
2 syndrome, osteogenesis imperfecta, acute intermittent porphyria,  
2 autoimmune diseases, inflammation, cancer, diseases of the nervous  
2 system, infection by pathogenic microorganisms, and characteristics such  
2 as longevity, appearance (e.g. baldness, obesity), strength, speed,  
2 endurance, fertility, and susceptibility or receptivity to particular  
2 drugs or therapeutic treatments. The isolated polymorphic nucleic acid  
2 segments can also be used to produce medicaments for the treatment or  
2 prophylaxis of such diseases  
K  
2 Sequence 210 BP; 24 A; 70 C; 79 G; 36 T; 0 U; 1 Other;

Query Match 100.0%; Score 36; DB 2; Length 210;  
Best Local Similarity 97.2%; Pred. No. 0.0025;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||:|||||  
o 80 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 115

RESULT 5  
EC91757  
D AEC91757 standard; DNA; 420 BP.  
K  
C AEC91757;  
K  
P 01-DEC-2005 (first entry)  
K  
E Template B3AR SEQ ID NO:33.  
K  
W DNA detection; SNP detection; template; ds.  
K  
S Synthetic.  
K  
N JP2005261354-A.  
K  
D 29-SEP-2005.  
K  
F 19-MAR-2004; 2004JP-00080974.  
K  
R 19-MAR-2004; 2004JP-00080974.  
K  
A (KYOT-) KYOTO DAIICHI KAGAKU KK.  
K  
I Inose K;  
K  
R WPI; 2005-662138/68.  
K  
P Detecting target nucleic acid, involves detecting target based on change  
P of fluorescence intensity due to formation or dissociation of hybrid of  
P target nucleic acid and hybridization probe having 5-carboxy fluorescein.  
K  
S Example 10; SEQ ID NO 33; 28pp; Japanese.  
V

THE INVENTION relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto hydrazide (Cascade blue). Also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a template sequence used in an example from the present invention.

Sequence 420 BP; 55 A; 148 C; 142 G; 74 T; 0 U; 1 Other;

Query Match 100.0%; Score 36; DB 14; Length 420;  
Best Local Similarity 97.2%; Pred. No. 0.0025;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CCTGCTGGTCATCGTGGCCATCGCCCGACTCCGAG 36  
|||||:|||||  
165 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 200

ESULT 6  
BK11513  
ABK11513 standard; DNA; 2040 BP.  
ABK11513;  
05-JUN-2002 (first entry)  
Human beta-3-adrenergic receptor (ADRB3) gene, generic sequence.  
Human; beta-3-adrenergic; receptor; ADRB3; anorectic; ds; antidiabetic;  
gene therapy; morbid obesity; insulin resistance;  
non-insulin-dependent diabetes mellitus; haplotyping; SNP;  
single nucleotide polymorphism.  
Homo sapiens.  
Synthetic.  
WO200208425-A2.  
31-JAN-2002.  
23-JUL-2001; 2001WO-US023223.  
21-JUL-2000; 2000US-0220088P.  
(GENA-) GENAISSANCE PHARM INC.  
Finkel K, Koshy B;  
WPI; 2002-241571/29.  
Novel genetic variants of beta-3-adrenergic receptor gene useful in  
studying expression and function of the protein, and for screening drugs

to treat diseases e.g. obesity, non insulin dependent diabetes mellitus.

Example 2; Page 90-91; 91pp; English.

The present invention relates to a new polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for ADRB3 (beta-3-adrenergic receptor) protein. The reference sequence comprises a sequence of 408 amino acids as given in the specification, or its fragment, and the polymorphic variant comprises one or more variant amino acids. The polymorphic variants are useful in studying the expression and function of ADRB3, in expressing ADRB3 protein for use in screening for candidate drugs to treat diseases related to ADRB3 activity, in studying the effect of the variation on the biological activity of ADRB3, and the binding affinity of candidate drugs targeting ADRB3 for the treatment of disorders such as morbid obesity, insulin resistance and an early onset of non-insulin-dependent diabetes mellitus. Haplotyping methods are useful in validating ADRB3 as a candidate target for treating a specific condition or disease predicted to be associated with ADRB3 activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with ADRB3 activity. The present nucleic acid sequence represents the human ADRB3 generic sequence representing all possible single nucleic polymorphisms (SNP) of the gene. This sequence was used in the methods of the invention to facilitate electronic searching of the ADRB3 haplotypes

Sequence 2040 BP; 140 A; 321 C; 351 G; 191 T; 0 U; 1037 Other;

Query Match 100.0%; Score 36; DB 6; Length 2040;  
Best Local Similarity 97.2%; Pred. No. 0.0027;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CCTGCTGGTCATCGTGGCCATCGCCCGACTCCGAG 36  
|||||:|||||  
485 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 520

RESULT 7  
ADZ42281  
ADZ42281 standard; DNA; 5669 BP.  
ADZ42281;  
14-JUL-2005 (first entry)  
Human beta-3 adrenoreceptor gene with T1387C SNP Seq 8.  
renal disease; nephrotropic; SNP detection;  
single nucleotide polymorphism; SNP; beta-3 adrenoreceptor; ds; gene.  
Homo sapiens.

Key	Location/Qualifiers
5'UTR	1001..1197 /*tag= a
CDS	1198..3449 /*tag= c /product= "Beta-3 adrenoreceptor protein"
exon	1198..2402 /*tag= b /number= 1
variation	1387 /*tag= d /standard_name= "Single nucleotide polymorphism"
intron	2403..3427 /*tag= e /number= 1
exon	3428..3449 /*tag= f /number= 2
3'UTR	3450..4669 /*tag= c



JP2005110606-A.  
28-APR-2005.  
.09-OCT-2003; 2003JP-00350959.  
09-OCT-2003; 2003JP-00350959.  
(KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.  
(DOKU-) DOKURITSU GYOSEI HOJIN IYAKUJIN IRYO KIK.  
WPI; 2005-326228/34.  
Testing hypertensive renal disease factor, by determining polymorphism in genotype of gene relevant to hypertensive renal disease, and estimating risk factor for hypertensive renal disease based on determined genotype, as index.  
Claim 1; SEQ ID NO 8; 440pp; Japanese.  
This invention relates to a novel method for testing hypertensive renal disease. Specifically, it refers to determining polymorphisms in the genotype of a gene relevant to hypertensive renal disease and estimating the risk factor for developing the disease accordingly. The present invention describes identifying gene polymorphisms in at least one of the following genes, namely endothelin converting-enzyme 1, mineralocorticoid receptor, urotensin II, superoxide-dismutase 3, thiazide sensitivity NaCl symporter, guanosine cyclase-A, hepatocyte growth factor, beta-3 adrenoreceptor, aldosterone synthetase, endothelium nitrogen monoxide synthetase, klotho and a sodium-calcium exchanger. Furthermore, it provides primers and probes for determining hypertensive renal disease factors, in particular in relation to renal diseases including hypertensive early renal disease and hypertensive kidney blood flow obstruction. The method enables detection of risk factors, and thus helps in preventing or delaying renal disease. This polynucleotide sequence is the full length human beta-3 adrenoreceptor gene given in an exemplification of the invention.  
Sequence 5669 BP; 1120 A; 1583 C; 1585 G; 1380 T; 0 U; 1 Other;

Query Match 100.0%; Score 36; DB 14; Length 5669;  
Best Local Similarity 97.2%; Pred. No. 0.0028;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||||:|||||  
1362 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 1397

ESULT 8  
BK11451  
ABK11451 standard; DNA; 10306 BP.  
ABK11451;  
05-JUN-2002 (first entry)  
Human beta-3-adrenergic receptor (ADRB3) gene sequence.  
Human; beta-3-adrenergic; receptor; ADRB3; gene; anorectic; antidiabetic; gene therapy; morbid obesity; insulin resistance; non-insulin-dependent diabetes mellitus; haplotyping; SNP; single nucleotide polymorphism; chromosome 8p12-p11\_2; ds.  
Homo sapiens.  
Key Location/Qualifiers  
variation replace(3574,A)  
/\*tag= a  
/\*standard name= "Single nucleotide polymorphism DS1"

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variation      replace(3901,C)
/*tag= b
/*standard_name= "Single nucleotide polymorphism, PS2"
variation      replace(3903,C)
/*tag= c
/*standard_name= "Single nucleotide polymorphism, PS3"
CDS            4056..6307
/*tag= d
/*product= "Human ADRB3 protein"
/*note= "Specifically claimed in claim 27"
exon           4056..5260
/*tag= e
/*number= 1
variation      replace(4109,G)
/*tag= f
/*standard_name= "Single nucleotide polymorphism, PS4"
variation      replace(4245,C)
/*tag= g
/*standard_name= "Single nucleotide polymorphism, PS5"
variation      replace(4436,T)
/*tag= h
/*standard_name= "Single nucleotide polymorphism, PS6"
variation      replace(4567,G)
/*tag= i
/*standard_name= "Single nucleotide polymorphism, PS7"
variation      replace(4849,T)
/*tag= j
/*standard_name= "Single nucleotide polymorphism, PS8"
variation      replace(4858,T)
/*tag= k
/*standard_name= "Single nucleotide polymorphism, PS9"
variation      replace(4887,A)
/*tag= l
/*standard_name= "Single nucleotide polymorphism, PS10"
variation      replace(5112,T)
/*tag= m
/*standard_name= "Single nucleotide polymorphism, PS11"
variation      replace(5183,T)
/*tag= n
/*standard_name= "Single nucleotide polymorphism, PS12"
intron         5261..6285
/*tag= o
/*number= 1
variation      replace(5274,T)
/*tag= p
/*standard_name= "Single nucleotide polymorphism, PS13"
variation      replace(5342,G)
/*tag= q
/*standard_name= "Single nucleotide polymorphism, PS14"
exon           6286..6307
/*tag= r
/*number= 2
variation      replace(6349,A)
/*tag= s
/*standard_name= "Single nucleotide polymorphism, PS15"
variation      replace(6557,C)
/*tag= t
/*standard_name= "Single nucleotide polymorphism, PS16"
variation      replace(6561,T)
/*tag= u
/*standard_name= "Single nucleotide polymorphism, PS17"

```

```

X
N WO200208425-A2.
X
D 31-JAN-2002.
X
F 23-JUL-2001; 2001WO-US023223.
X
R 21-JUL-2000; 2000US-0220088P.
X
A (CENA) GENAISANCE PHARM INC

```

1--Start Fragment-->RESULT 1

3-08-087-772A-14

Sequence 14, Application US/08087772A

Patent No. 5691155

GENERAL INFORMATION:

APPLICANT: Nahmias, Clara  
APPLICANT: Emorine, Jean L.  
APPLICANT: Strosberg, Donny A.  
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine  
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5691155th Carolina  
COUNTRY: USA  
ZIP: 28234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,772A  
FILING DATE:  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
NAME: Linker, Raymond O.  
REGISTRATION NUMBER: 26,419  
REFERENCE/DOCKET NUMBER: 3339-195

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1134 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

3-08-087-772A-14

Query Match 95.6%; Score 34.4; DB 2; Length 1134;  
Best Local Similarity 97.2%; Pred. No. 0.0021;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CCTGCTGGTCATCGTGGCCATCGCCCGACTCCGAG 36  
|||||  
o 165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200

RESULT 2

3-09-993-844A-13

Sequence 13, Application US/09993844A

Patent No. 7018812

GENERAL INFORMATION:

APPLICANT: Oakley, Robert H.  
APPLICANT: Barak, Lawrence S.  
APPLICANT: Laporte, Stephane A.  
APPLICANT: Caron, Marc G.  
TITLE OF INVENTION: Modified G-Protein Coupled Receptors  
FILE REFERENCE: 033072-026  
CURRENT APPLICATION NUMBER: US/09/993,844A  
CURRENT FILING DATE: 2001-11-05  
PRIOR APPLICATION NUMBER: US 60/245,772  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/260,363  
PRIOR FILING DATE: 2001-01-08  
NUMBER OF SEQ ID NOS: 82

SEQ ID NO: 1  
LENGTH: 1185  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: nucleotide sequence of beta3-AR-V2R chimera  
3-09-993-844A-13

Query Match 95.6%; Score 34.4; DB 5; Length 1185;  
Best Local Similarity 97.2%; Pred. No. 0.0021;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||  
o 165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200

ESULT 3  
3-07-916-901-1  
Sequence 1, Application US/07916901  
Patent No. 5364772

GENERAL INFORMATION:  
APPLICANT: Granneman, James G.  
APPLICANT: Lahners, Kristine N.  
APPLICANT: Rao, Donald D.  
TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA  
TITLE OF INVENTION: ENCODING SAME  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &  
ADDRESSEE: MILTON  
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390  
CITY: Troy  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48099

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/916,901  
FILING DATE: 19920720  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-324 (WSU)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (313) 689-3554

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1227 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1224

3-07-916-901-1

Query Match 95.6%; Score 34.4; DB 2; Length 1227;  
Best Local Similarity 97.2%; Pred. No. 0.0021;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||  
o 165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200

ESULT 4

3-08-351-473B-7

Sequence 7, Application US/08351473B

Patent No. 5656440

GENERAL INFORMATION:

APPLICANT: LENZEN, GERLINDA

APPLICANT: KAPOOR, ARCHANA

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE

TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/351,473B

FILING DATE: 21-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 93 04670

FILING DATE: 21-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR94/00447

FILING DATE: 21-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 6639-001-0X PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1227 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-351-473B-7

Query Match 95.6%; Score 34.4; DB 2; Length 1227;

Best Local Similarity 97.2%; Pred. No. 0.0021;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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      |||
o      165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200
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ESULT 5

3-09-016-434-1184

Sequence 1184, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INOVTE PHARMACEUTICALS INC

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1184:

SEQUENCE CHARACTERISTICS:

LENGTH: 1270 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: gl78895

3-09-016-434-1184

Query Match 95.6%; Score 34.4; DB 3; Length 1270;

Best Local Similarity 97.2%; Pred. No. 0.0021;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36  
|||||  
202 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 237

RESULT 6

3-08-450-962-1

Sequence 1, Application US/08450962

Patent No. 6274706

GENERAL INFORMATION:

APPLICANT: EMORINE, Laurent; MARULLO, Stefano;

APPLICANT: STROSBERG, Donny

TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND

TITLE OF INVENTION: GENES

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: KECK, MAHIN & CATE

STREET: P.O. BOX 06110

CITY: CHICAGO

STATE: ILLINOIS

COUNTRY: U.S.A.

ZIP: 60606-0110

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/2" diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,962

FILING DATE:

CLASSIFICATION: 520

APPLICATION NUMBER: 08/117,829

FILING DATE: 08-SEPT-1993

APPLICATION NUMBER: 07/721,571

FILING DATE: 25-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR89/00918

FILING DATE: 25-JAN-1989

ATTORNEY/AGENT INFORMATION:

NAME: Fleit, Martin; Gollin, Michael A.

REGISTRATION NUMBER: 16,900; 31,957

REFERENCE/DOCKET NUMBER: 47078-042

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 789-3400

TELEFAX: (202) 789-1158

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3683 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

3-08-450-962-1

Query Match 95.6%; Score 34.4; DB 3; Length 3683;

Best Local Similarity 97.2%; Pred. No. 0.0022;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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y      1 CCTGCTGGTCATCGTGGCCATCGCCCGACTCCGAG 36
      |||
o      802 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 837
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ESULT 7

!---EndFragment-->

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104107\_us-10-553-509- 10.szlrm60.rnpbm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104107\_us-10-53-509-10.szlrm60.rnpbm.

[Start](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
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4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 06:59:56 ; Search time 717.371 Seconds  
(without alignments)  
308.317 Million cell updates/sec

Title: US-10-553-509-10  
Effect score: 18  
Sequence: 1 catcgctggactccgag 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24217294

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
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8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
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11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
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2	18	100.0	41	8	US-10-398-445-7	Sequence 7, Appli
3	17.6	100.0	21	10	US-10-831-997-1650	Sequence 1650, Ap
4	17.6	100.0	29	7	US-10-336-638-896	Sequence 896, App
5	17.6	100.0	41	8	US-10-398-445-1	Sequence 1, Appli
6	17.6	100.0	42	10	US-10-730-771-38	Sequence 38, Appl
7	17	94.4	19	8	US-10-398-445-2	Sequence 2, Appli
8	16.4	91.1	22	3	US-09-257-650-3	Sequence 3, Appli
9	16.4	91.1	26	3	US-09-576-715A-8	Sequence 8, Appli
10	16.4	91.1	41	8	US-10-398-445-4	Sequence 4, Appli
11	16.4	91.1	41	8	US-10-398-445-6	Sequence 6, Appli
12	15.6	86.7	21	10	US-10-831-997-1651	Sequence 1651, Ap
13	15	83.3	25	8	US-10-719-956-681619	Sequence 681619,
14	14.8	82.2	25	11	US-10-933-982-178318	Sequence 178318,
15	14.8	82.2	25	13	US-11-036-317-482682	Sequence 482682,
16	14.4	80.0	25	6	US-10-098-263B-43003	Sequence 43003, A
17	14.4	80.0	25	6	US-10-098-263B-43631	Sequence 43631, A
18	14.4	80.0	25	15	US-11-121-849-250204	Sequence 250204,
19	14	77.8	25	9	US-10-719-900-374208	Sequence 374208,
20	13.8	76.7	19	14	US-11-083-784-1210384	Sequence 1210384,
21	13.8	76.7	19	15	US-11-101-244-1210384	Sequence 1210384,
22	13.8	76.7	25	6	US-10-098-263B-104983	Sequence 104983,
23	13.6	75.6	34	13	US-11-003-839-11	Sequence 11, Appl
24	13.6	75.6	34	16	US-11-230-462-11	Sequence 11, Appl
25	13.6	75.6	41	8	US-10-035-833A-3782	Sequence 3782, Ap
26	13.6	75.6	41	8	US-10-035-833A-3783	Sequence 3783, Ap
27	13.4	74.4	19	14	US-11-083-784-195789	Sequence 195789,
28	13.4	74.4	19	14	US-11-083-784-195891	Sequence 195891,
29	13.4	74.4	19	14	US-11-083-784-195989	Sequence 195989,
30	13.4	74.4	19	15	US-11-101-244-195789	Sequence 195789,
31	13.4	74.4	19	15	US-11-101-244-195891	Sequence 195891,
32	13.4	74.4	19	15	US-11-101-244-195989	Sequence 195989,
33	13.4	74.4	19	15	US-11-069-908-2272	Sequence 2272, Ap
34	13.4	74.4	19	15	US-11-069-908-4638	Sequence 4638, Ap
35	13.4	74.4	23	11	US-10-310-914A-940181	Sequence 940181,
36	13.4	74.4	25	8	US-10-719-956-59998	Sequence 59998, A
37	13.4	74.4	25	8	US-10-719-956-110194	Sequence 110194,
38	13.4	74.4	25	8	US-10-719-956-115498	Sequence 115498,
39	13.4	74.4	25	8	US-10-719-956-305844	Sequence 305844,
40	13.4	74.4	25	8	US-10-719-956-681620	Sequence 681620,
41	13.4	74.4	25	9	US-10-719-900-248512	Sequence 248512,
42	13.4	74.4	26	10	US-10-708-204-5426	Sequence 5426, Ap
43	13.4	74.4	27	10	US-10-708-204-5416	Sequence 5416, Ap
44	13.4	74.4	35	3	US-09-423-800-21	Sequence 21, Appl
45	13.4	74.4	35	6	US-10-182-018-21	Sequence 21, Appl

#### ALIGNMENTS

ESULT 1

3-10-398-445-5

Sequence 5, Application US/10398445

Publication No. US20040166498A1

#### GENERAL INFORMATION:

APPLICANT: PETERSON, RAYMOND J.

TITLE OF INVENTION: COMPUTER SYSTEM FOR DESIGNING OLIGONUCLEOTIDES USED IN

TITLE OF INVENTION: BIOCHEMICAL METHODS

FILE REFERENCE: 35804-188435

CURRENT APPLICATION NUMBER: US/10/398,445

CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: PCT/US01/31037

PRIOR FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/237,383

PRIOR FILING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 5

LENGTH: 41

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide

3-10-398-445-5

Query Match 100.0%; Score 18; DB 8; Length 41;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGAG 18  
|||||||  
o 14 CATCGCCTGGACTCCGAG 31

RESULT 2

3-10-398-445-7/c

Sequence 7, Application US/10398445

Publication No. US20040166498A1

GENERAL INFORMATION:

APPLICANT: PETERSON, RAYMOND J.

TITLE OF INVENTION: COMPUTER SYSTEM FOR DESIGNING OLIGONUCLEOTIDES USED IN

TITLE OF INVENTION: BIOCHEMICAL METHODS

FILE REFERENCE: 35804-188435

CURRENT APPLICATION NUMBER: US/10/398,445

CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: PCT/US01/31037

PRIOR FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/237,383

PRIOR FILING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 7

LENGTH: 41

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide

3-10-398-445-7

Query Match 100.0%; Score 18; DB 8; Length 41;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGAG 18  
|||||||  
o 28 CATCGCCTGGACTCCGAG 11

RESULT 3

3-10-831-997-1650

Sequence 1650, Application US/10831997

Publication No. US20050244834A1

GENERAL INFORMATION:

APPLICANT: Lander, Eric S.

APPLICANT: Cargill, Michele

APPLICANT: Ireland, James S.

APPLICANT: Bolk, Stacey

APPLICANT: Daley, George Q.

APPLICANT: McCarthy, Jeanette J.

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

FILE REFERENCE: 2825.1027-001

CURRENT APPLICATION NUMBER: US/10/831,997

CURRENT FILING DATE: 2004-04-26

PRIOR APPLICATION NUMBER: US/09/657,472

PRIOR FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/153,357

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US 60/220,947

PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: US 60/225,724

NUMBER OF SEQ ID NOS: 2551

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1650

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

3-10-831-997-1650

Query Match 100.0%; Score 18; DB 10; Length 21;

Best Local Similarity 94.4%; Pred. No. 38;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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y      1 CATCGCCTGGACTCCGAG 18
      |||||:|||||
o      4 CATCGCCYGGACTCCGAG 21
```

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104100\_us-10-553-509-10.szlmg60.rng.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104100\_us-10-53-509-10.szlmg60.rng.  
[Start](#) | [next page](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

Method: nucleic - nucleic search, using sw model

Run on: December 15, 2006, 05:57:43 ; Search time 217.011 Seconds  
(without alignments)  
578.313 Million cell updates/sec

Title: US-10-553-509-10  
Perfect score: 18  
Sequence: 1 catcgctggactccgag 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searches: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5397982

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8\*\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	18	100.0	18	10	20061214	20061214_104100_us-10-553-509-10.szlmg60.rng	

2	18	100.0	21	4	AAF96885	Aaf96885 Human gen
3	18	100.0	25	12	ADO26525	Ado26525 Novel hyb
4	18	100.0	26	6	ABL40567	Abl40567 Primer #7
5	18	100.0	34	13	ADT93453	Adt93453 Human bet
6	18	100.0	21	3	AAC73164	Aac73164 SNP flank
7	17.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
8	17.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
9	17.6	100.0	17	2	AAT58989	Aat58989 Obesity a
10	17	94.4	17	2	AAT58987	Aat58987 Obesity a
11	17	94.4	17	14	AEC91758	Aec91758 Probe 5T-
12	17	94.4	18	14	AEC91756	Aec91756 Probe 3T-
13	17	94.4	19	6	ABK50102	Abk50102 Allele sp
14	17	94.4	19	13	ADT93446	Adt93446 Fluoresce
15	16.4	91.1	25	6	ABL40568	Abl40568 Primer #8
16	16.4	91.1	25	12	ADO26526	Ado26526 Novel hyb
17	16.4	91.1	34	13	ADT93454	Adt93454 Human bet
18	16.4	91.1	41	6	ABK50104	Abk50104 Sense str
19	16.4	91.1	16	13	ADT93451	Adt93451 Fluoresce
20	16	88.9	21	4	AAF96886	Aaf96886 Human gen
21	16	88.9	17	2	AAT58988	Aat58988 Obesity a
22	15.4	85.6	17	2	AAT58990	Aat58990 Obesity a
23	15.4	85.6	21	14	AEC91760	Aec91760 Probe 3T-
24	15.4	85.6	51	4	AAH90342	Aah90342 Human clo
25	15.4	85.6	51	4	AAH90341	Aah90341 Human clo
26	15.4	85.6	15	13	ADT93452	Adt93452 Fluoresce
27	15	83.3	25	9	ACI43012	AcI43012 Human mic
28	14.4	80.0	25	9	ACI43640	AcI43640 Human mic
29	14.4	80.0	14	13	ADU50896	Adu50896 Human bet
30	14	77.8	14	14	ADZ42342	Adz42342 FAM probe
31	14	77.8	41	6	ABZ46998	Abz46998 Human ATP
32	14	77.8	41	6	ABZ46999	Abz46999 Human ATP
33	14	77.8	25	9	ACK05002	Ack05002 Human mic
34	13.8	76.7	34	2	AAV33317	Aav33317 Anti-CD23
35	13.6	75.6	16	13	ADT93445	Adt93445 Fluoresce
36	13.4	74.4	19	14	AEC28618	Aec28618 Human all
37	13.4	74.4	19	14	AEC26252	Aec26252 Human all
38	13.4	74.4	25	4	AAC89164	Aac89164 Sample DN
39	13.4	74.4	33	2	AAQ87254	Aaq87254 Primer fo
40	13.4	74.4	35	2	AAV24264	Aav24264 Chimeric
41	13.4	74.4	35	2	AAX00108	Aax00108 Human ant
42	13.4	74.4	35	3	AAZ58889	Aaz58889 PCR prime
43	13.4	74.4	35	4	AAF69217	Aaf69217 Chimeric
44	13.4	74.4	35	4	AAF69105	Aaf69105 Chimeric
45	13.4	74.4				

ALIGNMENTS

ESULT 1  
DT93450  
D ADT93450 standard; DNA; 18 BP.  
K  
C ADT93450;  
K  
T 13-JAN-2005 (first entry)  
K  
E Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.  
K  
W SNP detection; beta3 adrenaline receptor; ss; probe.  
K  
S Homo sapiens.  
K  
H Key Location/Qualifiers  
T modified\_base 1  
T /\*tag= a  
T /mod\_base= OTHER  
T /note= "OTHER = Linked to BODIPY FL group"  
T modified\_base 18  
T /\*tag= b  
T /mod\_base= OTHER

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 2; SEQ ID NO 10; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the fluorescent-labelled probe (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline receptor (B3AR) T190 variant DNA.

Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred: No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CATCGCCTGGACTCCGAG 18
  |||||
1 CATCGCCTGGACTCCGAG 18
    
```

ESULT 2

DT93449

ADT93449 standard; DNA; 20 BP.

ADT93449;

13-JAN-2005 (first entry)

Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.

SNP detection; beta3 adrenaline receptor; ss; probe.

Homo sapiens.

Key	Location/Qualifiers
modified_base	1
	/*tag= a
	/mod_base= OTHER
	/note= "OTHER = Linked to BODIPY FL group"
modified_base	20
	/*tag= b
	/mod_base= OTHER
	/note= "OTHER = Linked to B group"

WO2004092385-A1.  
28-OCT-2004.  
16-APR-2004; 2004WO-JP005525.  
18-APR-2003; 2003JP-00114381.  
(ARKR-) ARKRAY INC.  
Hirai M;  
WPI; 2004-784610/77.  
Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
receptor gene having single nucleotide polymorphism, labeled at terminal  
with fluorescent dye and shows decrease in fluorescence of fluorescent  
dye upon hybridization.  
Claim 2; SEQ ID NO 9; 31pp; Japanese.  
The invention relates to a novel nucleic acid probe which is labelled at  
a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
of the fluorescent dye is observed upon hybridisation. The probe  
comprises a base sequence derived from a fully defined sequence of 1227  
nucleotides as given in the specification and being labelled at the 3' or  
5' end with a fluorescent dye. The probe of the invention may be useful  
for detecting a mutation or single nucleotide polymorphism (SNP) in the  
beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
contamination of the amplified product is prevented and the process is  
automated. The current sequence is that of the fluorescent-labelled probe  
(SEQ ID 5) of the invention which was targeted to human beta3 adrenaline  
receptor (B3AR) T190 variant DNA.  
Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||  
1 CATCGCCTGGACTCCGAG 18

ESULT 3  
AF96885  
AAF96885 standard; DNA; 21 BP.  
AAF96885;  
18-NOV-2004 (revised)  
06-JUN-2001 (first entry)  
Human gene single nucleotide polymorphism #1646.  
Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
polymorphism; vascular disease; coronary artery disease; forensics;  
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
pulmonary embolism; paternity test; ds.  
Homo sapiens.  
Unidentified.  
Key Location/Qualifiers  
variation 11  
/\*tag= a  
/standard\_name= "Single nucleotide polymorphism"

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.

26-JUL-2000; 2000US-0220947P.

16-AUG-2000; 2000US-0225724P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;

WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.

Example; Page 159; 242pp; English.

The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPs shown in the specification

Revised record issued on 18-NOV-2004 : The variation feature was incorrectly given a capital V

Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||  
4 CATCGCCTGGACTCCGAG 21

ESULT 4

DO26525

ADO26525 standard; DNA; 25 BP.

ADO26525;

12-AUG-2004 (first entry)

Novel hybridisation detection-related oligonucleotide SeqID1.

hybridisation detection; immobilised probe; AC impedance;  
foetal genome analysis; ss.

Unidentified.

WO2004044570-A1.

27-MAY-2004.

30-SEP-2003; 2003WO-JP012499.

WO200118250 # 21



(TOYA-) TOYAMA PREFECTURE.  
(COSE-) COSEL CO LTD.  
(TATE-) TATEYAMA KAGAKU IND CO LTD.  
(TOXX ) TOYO KAKO CO LTD.

Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;  
Nakagawa A, Mizuhara T, Mizushima M, Nakada M;

WPI; 2004-420427/39.

Detection of hybridization of an immobilized probe to a target nucleic acid by measuring AC impedance across the carrier surface for specific gene detection in investigation and diagnosis of disease.

Example; SEQ ID NO 1; 33pp; Japanese.

This invention relates to a novel method of detecting hybridisation of an immobilised probe to a target nucleic acid using measurement of AC impedance. Detection of specific genes and gene sequences in nucleic acid samples (such as samples of genomic DNA) may be useful for diagnosis, prediction and prevention of genetic disorders and analysis of foetal genome. Hybridisation is detected with high accuracy and sensitivity without the use of dyes. The present sequence is that of an oligonucleotide which was used in the exemplification of the invention.

Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||  
6 CATCGCCTGGACTCCGAG 23

ESULT 5  
3L40567

ABL40567 standard; DNA; 26 BP.

ABL40567;

17-JUN-2002 (first entry)

Primer #7 used in a base polymorphism detection method.

Polymorphism; nucleic acid detection; endonuclease; probe; ADRB2;  
hybridisation; PCR primer; ss.

Synthetic.

JP2002034598-A.

05-FEB-2002.

27-JUL-2000; 2000JP-00226912.

27-JUL-2000; 2000JP-00226912.

(TOYM ) TOYOBO KK.

WPI; 2002-298820/34.

Detection of base polymorphism.

Disclosure; Page 10; 10pp; Japanese.

The invention relates to a method for detecting base polymorphism. The method involves (1) amplifying the nucleic acid fragment containing base

polymorphism of the specific nucleic acid sequence; (2) hybridizing the amplified nucleic acid with at least two polymorphism-specific probes; (3) treating with RNA-selective cleavage endonuclease; (4) measuring detecting signals of each probe; and (5) identifying polymorphism by the ratio of each detecting signals. The probe can be used for detecting base polymorphism. The present sequence represents a PCR primer used in the course of the invention

Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||  
9 CATCGCCTGGACTCCGAG 26

RESULT 6  
DT93453

ADT93453 standard; DNA; 34 BP.

ADT93453;

13-JAN-2005 (first entry)

Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.

single nucleotide polymorphism; SNP; SNP detection;  
beta3 adrenaline receptor; ds.

Homo sapiens.

Key Location/Qualifiers  
variation replace(19,C)  
/\*tag= a  
/standard\_name= "Single nucleotide polymorphism"

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Example 1; Fig 1; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the human beta3 adrenaline

1 Accepted (BANK) 1150 variant DNA fragments of the invention.

2 Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 34;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||  
12 CATCGCCTGGACTCCGAG 29

RESULT 7  
AC73164  
D AAC73164 standard; DNA; 21 BP.  
K  
C AAC73164;  
K  
T 02-FEB-2001 (first entry)  
K  
E SNP flanking sequence #24 used in multiplexing PCR/SBE assay.  
K  
W Oligonucleotide array; genotyping; single base extension reaction; SBE;  
W polymorphic locus; single nucleotide polymorphism; ss.  
K  
S Unidentified.  
K  
N WO200058516-A2.  
K  
D 05-OCT-2000.  
K  
F 27-MAR-2000; 2000WO-US008069.  
K  
R 26-MAR-1999; 99US-0126473P.  
R 23-JUN-1999; 99US-0140359P.  
K  
A (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
A (AFFY-) AFFYMETRIX INC.  
K  
I Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;  
I Ryder T, Sklar P;  
K  
R WPI; 2000-656171/63.  
K  
T Universal array of oligonucleotides tags attached to a solid substrate  
T along with locus-specific tagged oligonucleotides useful in genotyping  
T using single base extension reactions.  
K  
S Example 7; Page 50; 70pp; English.  
K  
C The present invention relates to an oligonucleotide array comprising  
C oligonucleotide tags fixed to a solid substrate. The oligonucleotide  
C array is useful for genotyping a nucleic acid sample at one or more loci  
C via single base extension (SBE) reactions. A pair of primers is used to  
C amplify a polymorphic locus in a sample e.g. a single nucleotide  
C polymorphism (SNP). The present sequence is one such polymorphic locus  
C used in the present invention. The amplified nucleic acid product is then  
C used as a template in a SBE reaction with an extension primer. The SBE  
C reaction products are used to form the oligonucleotide array. Note: This  
C sequence includes a SNP represented by the degenerate codon in the  
C sequence  
K  
2 Sequence 21 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 1 Other;

Query Match 100.0%; Score 18; DB 3; Length 21;  
Best Local Similarity 94.4%; Pred. No. 51;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||

ESULT 8

AA04696

D AAA04696 standard; DNA; 29 BP.

K

C AAA04696;

K

I 22-MAY-2000 (first entry)

K

E Polymorphic fragment of hypertension associated gene ADRB3.

K

N Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
N Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
N Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;  
N polycystic kidney disease; von Willebrands disease; forensic; human;  
N tuberous sclerosis; hereditary hemorrhagica telangiectasia;  
N familial colonic polyposis; osteogenesis imperfecta; porphyria;  
N Ehlers-Danlos syndrome; ss.

K

S Homo sapiens.

K

N EP955382-A2.

K

D 10-NOV-1999.

K

F 07-MAY-1999; 99EP-00250150.

K

R 07-MAY-1998; 98US-0084641P.

R

R 03-MAY-1999; 99US-00304232.

K

A (AFFY-) AFFYMETRIX INC.

A

A (UYCA-) UNIV CASE WESTERN RESERVE.

K

I Fan JB, Chakravarti A, Haluska MK;

K

R WPI; 2000-107928/10.

K

I Novel nucleic acids containing polymorphisms used in the diagnosis of  
I hypertension.

K

S Disclosure; Page 45; 53pp; English.

K

C The invention provides polymorphic fragments of genes associated with  
C hypertension. The nucleic acids including the polymorphic sites can be  
C used as probes or primers for expressing variant proteins. Detection of  
C the polymorphisms is useful in designing prophylactic and therapeutic  
C regimes customized to underlying abnormalities. The polymorphisms can be  
C used for association studies for hypertension, and in hypertension  
C diagnostic assays. Where the polymorphisms have strong correlation with  
C hypertension, within a gene, they are likely to have a causative role in  
C hypertension. This information can be used to find the precise role of a  
C polymorphism in the disease, and this can be used to identify potential  
C drugs which combat the disease. The polymorphisms can be tested for  
C association with other diseases e.g. agammaglobulinemia, diabetes  
C insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
C syndrome, Fabrys disease, familial hypercholesterolemia, polycystic  
C kidney disease, hereditary spherocytosis, von Willebrands disease,  
C tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial  
C colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
C acute intermittent porphyria. The polymorphic forms can also be used in  
C forensics to identify individuals

K

Q Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 18; DB 3; Length 29;

Best Local Similarity 94.4%; Pred. No. 51;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ESULT 9

3K50101

ABK50101 standard; DNA; 41 BP.  
 ABK50101;  
 15-JUL-2002 (first entry)  
 Nucleic acid sequence used for sequence formatting.  
 Optimal reagent oligonucleotide; target nucleic acid evaluation;  
 target feature; exclusion value; ranking value; sequence window;  
 sequence formatting; ds.  
 Synthetic.  
 WO200229379-A2.  
 11-APR-2002.  
 04-OCT-2001; 2001WO-US031037.  
 04-OCT-2000; 2000US-0237383P.  
 (CELA-) CELADON LAB INC.  
 Peterson RJ;  
 WPI; 2002-340129/37.  
 Determining an optimal reagent oligonucleotide for evaluating a target  
 nucleic acid having a target feature, involves defining a set of  
 exclusion values and/or ranking values specific to a biochemical method.  
 Example; Fig 1B; 91pp; English.  
 The present invention relates to a new method for determining an optimal  
 reagent oligonucleotide for evaluating a target nucleic acid having a  
 target feature. The method comprises defining a set of exclusion values  
 and/or ranking values specific to the method, defining a sequence window  
 adjacent to the target, and generating candidate reagent oligonucleotides  
 complementary to the sense and/or antisense strands of the target within  
 the window. The method can be used for determining an optimal reagent  
 oligonucleotide sequence for use in a biochemical method for evaluating a  
 target nucleic acid sequence having a target feature. The present nucleic  
 acid sequence represent a DNA molecule used in the methods of the  
 invention for nucleic acid sequence formatting  
 Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;

Query Match 100.0%; Score 18; DB 6; Length 41;  
 Best Local Similarity 94.4%; Pred. No. 52;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
 |||||:|||||||  
 14 CATCGCCYGGACTCCGAG 31

ESULT 10

AT58989

AAT58989 standard; DNA; 17 BP.  
 AAT58989;  
 04-AUG-1997 (first entry)

Obesity; and type II diabetes mellitus diagnosis target nucleic acid probe.  
Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;  
beta3AR; ss.  
Synthetic.  
WO9636641-A1.  
21-NOV-1996.  
17-MAY-1996; 96WO-US007218.  
19-MAY-1995; 95US-00446530.  
(UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.  
Shuldiner AR, Walston J, Silver K, Roth J;  
WPI; 1997-012034/01.  
New isolated beta3-adrenergic receptor mutation - used to develop prods.  
for the diagnosis and treatment of type II diabetes and/or obesity.  
Claim 17; Page 42; 51pp; English.  
The present sequence is a nucleic acid probe used in a method for  
diagnosis of a subject having or at risk of having type II diabetes  
mellitus and/or obesity. The method involves contacting a target nucleic  
acid of a sample from the subject with a nucleic acid probe (preferably  
the present sequence or that in AAT58990) that detects a mutation in the  
beta3-adrenergic receptor (beta3AR) gene. The present sequence can also  
be used in the treatment of subjects having or at risk of having type II  
diabetes and/or obesity  
Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGA 17  
|||||||  
1 CATCGCCTGGACTCCGA 17

ESULT 11  
AT58987/c  
AAT58987 standard; DNA; 17 BP.  
AAT58987;  
04-AUG-1997 (first entry)  
Obesity and type II diabetes mellitus diagnosis target nucleic acid.  
Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;  
beta3AR; ss.  
Synthetic.  
WO9636641-A1.  
21-NOV-1996.  
17-MAY-1996; 96WO-US007218.  
19-MAY-1995; 95US-00446530.  
(UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.

X  
R .WPI; 1997-012034/01.  
X  
T New isolated beta3-adrenergic receptor mutation - used to develop prods.  
T for the diagnosis and treatment of type II diabetes and/or obesity.  
X  
S Claim 16; Page 42; 51pp; English.  
X  
C The present sequence is a target nucleic acid detected in a method for  
C diagnosis of a subject having or at risk of having type II diabetes  
C mellitus and/or obesity. The method involves contacting a target nucleic  
C acid of a sample from the subject (preferably the present sequence or  
C that in AAT58988) with a nucleic acid probe that detects a mutation in  
C the beta3-adrenergic receptor (beta3AR) gene  
X  
Q Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGA 17  
|||  
O 17 CATCGCCTGGACTCCGA 1

ESULT 12  
EC91758/c  
O AEC91758 standard; DNA; 17 BP.

X  
C AEC91758;  
X  
T 01-DEC-2005 (first entry)  
X  
E Probe 5T-B3AR-w-IMS-R2-17 SEQ ID NO:34.  
X  
W DNA detection; SNP detection; probe; ss.  
X  
S Synthetic.

X  
N JP2005261354-A.  
X  
O 29-SEP-2005.  
X  
F 19-MAR-2004; 2004JP-00080974.  
X  
R 19-MAR-2004; 2004JP-00080974.  
X  
A (KYOT-) KYOTO DAIICHI KAGAKU KK.  
X  
I Inose K;  
X  
R WPI; 2005-662138/68.

T Detecting target nucleic acid, involves detecting target based on change  
T of fluorescence intensity due to formation or dissociation of hybrid of  
T target nucleic acid and hybridization probe having 5-carboxy fluorescein.

S Example 10; SEQ ID NO 34; 28pp; Japanese.

C The invention relates to a method (M1) for detecting a target nucleic  
C acid. (M1) involves measuring the change of fluorescence intensity due to  
C formation or dissociation of the hybrid of the hybridization probe  
C comprising a labeled terminal portion, and a target nucleic acid, and  
C detecting the target nucleic acid based on the change, where the  
C hybridization probe is labeled using the fluorescent pigment chosen from  
C 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora  
C -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-  
C dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),  
C 5-carboxy rhodamine (BOY) and 1,2,6,8-tetrakis(4-sulfamoylphenyl)pyrene

hybridization (cascade blue; also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a probe used in an example from the present invention.

Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 14; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 CATCGCCTGGACTCCGA 17
  |||||
17 CATCGCCTGGACTCCGA 1
  
```

RESULT 13  
 EC91756/c

AEC91756 standard; DNA; 18 BP.

AEC91756;

01-DEC-2005 (first entry).

Probe 3T-B3AR-w-IMS-R1-18 SEQ ID NO:32.

DNA detection; SNP detection; probe; ss.

Synthetic.

JP2005261354-A.

29-SEP-2005.

19-MAR-2004; 2004JP-00080974.

19-MAR-2004; 2004JP-00080974.

(KYOT-) KYOTO DAIICHI KAGAKU KK.

Inose K;

WPI; 2005-662138/68.

Detecting target nucleic acid, involves detecting target based on change of fluorescence intensity due to formation or dissociation of hybrid of target nucleic acid and hybridization probe having 5-carboxy fluorescein.

Example 10; SEQ ID NO 32; 28pp; Japanese.

The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy X rhodamine (ROX) and 1-(2,6-dimethyl-5-sulfo-1-pyrenyl)ethylacetate



hybridization (cascade blue), also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a probe used in an example from the present invention.

Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

      2 ATCGCCTGGACTCCGAG 18
      |||||
     18 ATCGCCTGGACTCCGAG 2

```

RESULT 14

3K50102

ABK50102 standard; DNA; 19 BP.

ABK50102;

15-JUL-2002 (first entry)

Allele specific hybridisation probe.

Optimal reagent oligonucleotide; target nucleic acid evaluation;  
target feature; exclusion value; ranking value; sequence window;  
hybridisation; probe; ss.

Synthetic.

WO200229379-A2.

11-APR-2002.

04-OCT-2001; 2001WO-US031037.

04-OCT-2000; 2000US-0237383P.

(CELA-) CELADON LAB INC.

Peterson RJ;

WPI; 2002-340129/37.

Determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature, involves defining a set of exclusion values and/or ranking values specific to a biochemical method.

Example; Fig 2A; 91pp; English.

The present invention relates to a new method for determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature. The method comprises defining a set of exclusion values and/or ranking values specific to the method, defining a sequence window adjacent to the target, and generating candidate reagent oligonucleotides complementary to the sense and/or antisense strands of the target within the window. The method can be used for determining an optimal reagent oligonucleotide sequence for use in a biochemical method for evaluating a

acid sequence represent an allele specific hybridisation probe that was  
used in the methods of the invention in numbering systems

Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGA 17  
||||||||||||||  
3 CATCGCCTGGACTCCGA 19

ESULT 15  
DT93446  
ADT93446 standard; DNA; 19 BP.  
ADT93446;

[tart](#) | [next page](#)

---Start Fragment--->RESULT 1

BD107586  
ACUS BD107586 26 bp DNA linear PAT 18-SEP-2002  
DEFINITION Method for detecting base polymorphism.  
ACCESSION BD107586  
VERSION BD107586.1 GI:23202404  
KEYWORDS JP 2002034598-A/7.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Yoshiga,S., Takarada,Y., Aono,T. and Segawa,M.  
TITLE Method for detecting base polymorphism  
JOURNAL Patent: JP 2002034598-A 7 05-FEB-2002;  
TOYOBO CO LTD  
COMMENT OS Artificial Sequence  
PN JP 2002034598-A/7  
PD 05-FEB-2002  
PF 27-JUL-2000 JP 2000226912  
PI SATOKO YOSHIGA,YUTAKA TAKARADA,TOSHIYA AONO,MASAYA SEGAWA PC  
C12Q1/68,C12N9/22,C12N15/09,C12N15/00  
CC Description of Artificial Sequence:primer  
FH Key Location/Qualifiers  
FT source 1. .26  
FT /organism='Artificial Sequence'.  
FEATURES Location/Qualifiers  
source 1. .26  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||  
9 CATCGCCTGGACTCCGAG 26

RESULT 2  
R530447  
ACUS AR530447 21 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 1650 from patent US 6727063.  
ACCESSION AR530447  
VERSION AR530447.1 GI:53918884  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and  
McCarthy,J.J.  
TITLE Single nucleotide polymorphisms in genes  
JOURNAL Patent: US 6727063-A 1650 27-APR-2004;  
Millennium Pharmaceuticals, Inc. and Whitehead Institute for  
Biomedical Research; Cambridge, MA  
FEATURES Location/Qualifiers  
source 1. .21  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||:|||||||  
CATCGCCTGGACTCCGAG 21

ESULT 3  
K096472  
JCUS AX096472 21 bp DNA linear PAT 30-MAR-2001  
EFINITION Sequence 1650 from Patent WO0118250.  
JCESSION AX096472  
ERSION AX096472.1 GI:13512726  
EYWORDS  
JURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
EFERENCE 1  
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and  
Mccarthy,J.J.  
TITLE Single nucleotide polymorphisms in genes  
JOURNAL Patent: WO 0118250-A 1650 15-MAR-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium  
Pharmaceuticals, Inc. (US)  
EATURES Location/Qualifiers  
source 1. .21  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
RIGIN  
Query Match 100.0%; Score 18; DB 2; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
y 1 CATCGCCTGGACTCCGAG 18  
||||||:|||||||  
o 4 CATGCCCYGGACTCCGAG 21  
!---EndFragment-->

--Start Fragment-->RESULT 1

3-09-304-232-896  
Sequence 896, Application US/09304232  
Patent No. 6525185

9

GENERAL INFORMATION:  
APPLICANT: Fan, Jian Bing  
APPLICANT: Chakravarti, Aravinda  
APPLICANT: Halushka, Marc Kenneth  
APPLICANT: Case Western Reserve University School of Medicine  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Polymorphisms Associated With  
TITLE OF INVENTION: Hypertension  
FILE REFERENCE: 018547-034210US  
CURRENT APPLICATION NUMBER: US/09/304,232  
CURRENT FILING DATE: 1999-05-03  
EARLIER APPLICATION NUMBER: US 60/084,641  
EARLIER FILING DATE: 1998-05-07  
NUMBER OF SEQ ID NOS: 909  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 896  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ADRB3EX1 416

3-09-304-232-896

Query Match 100.0%; Score 20; DB 3; Length 29;  
Best Local Similarity 95.0%; Pred. No. 2.1;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAGAC 20  
|||||||:|||||||  
8 CATCGCCYGGACTCCGAGAC 27

RESULT 2  
3-09-657-472-1650  
Sequence 1650, Application US/09657472  
Patent No. 6727063

GENERAL INFORMATION:  
APPLICANT: Lander, Eric S.  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Bolk, Stacey  
APPLICANT: Daley, George Q.  
APPLICANT: McCarthy, Jeanette J.  
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES  
FILE REFERENCE: 2825.1027-001  
CURRENT APPLICATION NUMBER: US/09/657,472  
CURRENT FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/153,357  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 60/220,947  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: US 60/225,724  
PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 2551  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1650  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens

3-09-657-472-1650

Query Match 88.0%; Score 17.6; DB 3; Length 21;  
Best Local Similarity 94.4%; Pred. No. 20;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||

ESULT 3

3-09-657-472-1651

Sequence 1651, Application US/09657472

Patent No. 6727063

GENERAL INFORMATION:

APPLICANT: Lander, Eric S.

APPLICANT: Cargill, Michele

APPLICANT: Ireland, James S.

APPLICANT: Bolk, Stacey

APPLICANT: Daley, George Q.

APPLICANT: McCarthy, Jeanette J.

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

FILE REFERENCE: 2825.1027-001

CURRENT APPLICATION NUMBER: US/09/657,472

CURRENT FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/153,357

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US 60/220,947

PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: US 60/225,724

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2551

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1651

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

3-09-657-472-1651

Query Match 88.0%; Score 17.6; DB 3; Length 21;

Best Local Similarity 94.4%; Pred. No. 20;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

3 TCGCCTGGACTCCGAGAC 20

|||||||:|||||||

1 TCGCCTGGACWCCGAGAC 18

ESULT 4

3-08-446-530-5/c

Sequence 5, Application US/08446530

Patent No. 5766851

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.

APPLICANT: Walston, Jeremy

APPLICANT: Silver, Kristi

TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE

TITLE OF INVENTION: II DIABETES MELLITUS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,530

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 20 247

REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-446-530-5

Query Match 85.0%; Score 17; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
y      1 CATCGCCTGGACTCCGA 17
      ||||||||||||||||
o     17 CATCGCCTGGACTCCGA 1
```

RESULT 5

3-08-446-530-7

Sequence 7, Application US/08446530

Patent No. 5766851

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.

APPLICANT: Walston, Jeremy

APPLICANT: Silver, Kristi

TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE

TITLE OF INVENTION: II DIABETES MELLITUS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,530

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-446-530-7

Query Match 85.0%; Score 17; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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y      1 CATCGCCTGGACTCCGA 17
      ||||||||||||||||
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ESULT 6  
3-09-097-562-5/c  
Sequence 5, Application US/09097562  
Patent No. 5877283

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,562  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,530  
FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-09-097-562-5

Query Match 85.0%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGA 17  
|||||||  
17 CATCGCCTGGACTCCGA 1

ESULT 7  
3-09-097-562-7  
Sequence 7, Application US/09097562  
Patent No. 5877283

GENERAL INFORMATION:

APPLICANT: Shuldiner, Alan R.  
APPLICANT: Walston, Jeremy  
APPLICANT: Silver, Kristi  
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE  
TITLE OF INVENTION: II DIABETES MELLITUS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.



CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,562  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,530  
FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/048001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-09-097-562-7

Query Match 85.0%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGA 17  
|||||||  
1 CATCGCCTGGACTCCGA 17

!--EndFragment-->

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104100\_us-10-553-509- 9.szlm60.rng.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104100\_us-10-53-509-9.szlm60.rng.

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[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 05:57:43 ; Search time 241.124 Seconds  
(without alignments)  
578.313 Million cell updates/sec

Title: US-10-553-509-9  
Perfect score: 20  
Sequence: 1 catcgctggactccgagac 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5397982

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100%	20	12	12502440 Fluorim...

2	20	100.0	25	12	ADO26526	Ado26526 Novel hyb
3	20	100.0	34	13	ADT93453	Adt93453 Human bet
4	19.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
5	19.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
6	18.4	92.0	25	12	ADO26526	Ado26526 Novel hyb
7	18.4	92.0	34	13	ADT93454	Adt93454 Human bet
8	18.4	92.0	41	6	ABK50104	Abk50104 Sense str
9	18	90.0	18	13	ADT93450	Adt93450 Fluoresce
10	18	90.0	18	14	AEC91756	Aec91756 Probe 3T-
11	18	90.0	21	4	AAF96886	Aaf96886 Human gen
12	18	90.0	21	4	AAF96885	Aaf96885 Human gen
13	18	90.0	26	6	ABL40567	Abl40567 Primer #7
14	17.6	88.0	21	3	AAC73164	Aac73164 SNP flank
15	17	85.0	17	2	AAT58989	Aat58989 Obesity a
16	17	85.0	17	2	AAT58987	Aat58987 Obesity a
17	17	85.0	17	14	AEC91758	Aec91758 Probe 5T-
18	17	85.0	19	6	ABK50102	Abk50102 Allele sp
19	16.4	82.0	19	13	ADT93446	Adt93446 Fluoresce
20	16.4	82.0	25	6	ABL40568	Abl40568 Primer #8
21	16	80.0	16	13	ADT93451	Adt93451 Fluoresce
22	15.4	77.0	17	2	AAT58988	Aat58988 Obesity a
23	15.4	77.0	17	2	AAT58990	Aat58990 Obesity a
24	15.4	77.0	21	14	AEC91760	Aec91760 Probe 3T-
25	15.4	77.0	51	4	AAH90342	Aah90342 Human clo
26	15.4	77.0	51	4	AAH90341	Aah90341 Human clo
27	15	75.0	15	13	ADT93452	Adt93452 Fluoresce
28	14.8	74.0	25	9	ACK05002	Ack05002 Human mic
29	14.4	72.0	25	9	ACI43012	Aci43012 Human mic
30	14.4	72.0	25	9	ACI43640	Aci43640 Human mic
31	14.4	72.0	25	9	ACK29689	Ack29689 Human mic
32	14.2	71.0	25	9	ACI08822	Aci08822 Human mic
33	14.2	71.0	48	10	ADJ80399	Adj80399 Hybrid hu
34	14	70.0	14	13	ADU50896	Adu50896 Human bet
35	14	70.0	14	14	ADZ42342	Adz42342 FAM probe
36	14	70.0	41	6	ABZ46998	Abz46998 Human ATP
37	14	70.0	41	6	ABZ46999	Abz46999 Human ATP
38	13.8	69.0	21	13	ADU31703	Adu31703 Knock-dow
39	13.6	68.0	25	12	ADP13719	Adp13719 Renal cel
40	13.6	68.0	34	2	AAV33317	Aav33317 Anti-CD23
41	13.6	68.0	50	4	AAH89585	Aah89585 Human col
42	13.6	68.0	51	4	AAL27124	Aal27124 Human SNP
43	13.6	68.0	60	14	AED87834	Aed87834 Rabbit ty
44	13.4	67.0	16	13	ADT93445	Adt93445 Fluoresce
45	13.4	67.0	19	10	ADF83960	Adf83960 Human bre

# ALIGNMENTS

```

ESULT 1
DT93449
D   ADT93449 standard; DNA; 20 BP.
X
C   ADT93449;
X
T   13-JAN-2005   (first entry)
X
E   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.
X
W   SNP detection; beta3 adrenaline receptor; ss; probe.
X
S   Homo sapiens.
X
H   Key          Location/Qualifiers
T   modified_base 1
T                      /*tag= a
T                      /mod_base= OTHER
T                      /note= "OTHER = Linked to BODIPY FL group"
T   modified_base 20
T                      /*tag= b
T                      /mod_base= OTHER

```

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 2; SEQ ID NO 9; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of contamination of the amplified product is prevented and the process is automated. The current sequence is that of the fluorescent-labelled probe (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline receptor (B3AR) T190 variant DNA.

Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAGAC 20  
|||||||  
1 CATCGCCTGGACTCCGAGAC 20

# RESULT 2

DO26525

ADO26525 standard; DNA; 25 BP.

ADO26525;

12-AUG-2004 (first entry)

Novel hybridisation detection-related oligonucleotide SeqID1.

hybridisation detection; immobilised probe; AC impedance;  
foetal genome analysis; ss.

Unidentified.

WO2004044570-A1.

27-MAY-2004.

30-SEP-2003; 2003WO-JP012499.

14-NOV-2002; 2002JP-00331059.

(COSE-) COSEL CO LTD.  
(TATE-) TATEYAMA KAGAKU IND CO LTD.  
(TOXX ) TOYO KAKO CO LTD.

Teřasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;  
Nakagawa A, Mizuhara T, Mizushima M, Nakada M;

WPI; 2004-420427/39.

Detection of hybridization of an immobilized probe to a target nucleic acid by measuring AC impedance across the carrier surface for specific gene detection in investigation and diagnosis of disease.

Example; SEQ ID NO 1; 33pp; Japanese.

This invention relates to a novel method of detecting hybridisation of an immobilised probe to a target nucleic acid using measurement of AC impedance. Detection of specific genes and gene sequences in nucleic acid samples (such as samples of genomic DNA) may be useful for diagnosis, prediction and prevention of genetic disorders and analysis of foetal genome. Hybridisation is detected with high accuracy and sensitivity without the use of dyes. The present sequence is that of an oligonucleotide which was used in the exemplification of the invention.

Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAGAC 20  
|||||||  
6 CATCGCCTGGACTCCGAGAC 25

ESULT 3  
DT93453

ADT93453 standard; DNA; 34 BP.

ADT93453;

13-JAN-2005 (first entry)

Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.

single nucleotide polymorphism; SNP; SNP detection;  
beta3 adrenaline receptor; ds.

Homo sapiens.

Key Location/Qualifiers  
variation replace(19,C)  
/\*tag= a  
/standard\_name= "Single nucleotide polymorphism"

WO2004092385-A1

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline

1 receptor gene having single nucleotide polymorphism, labeled at terminal  
T with fluorescent dye and shows decrease in fluorescence of fluorescent  
T dye upon hybridization.

3 Example 1; Fig 1; 31pp; Japanese.

2 The invention relates to a novel nucleic acid probe which is labelled at  
2 a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
2 of the fluorescent dye is observed upon hybridisation. The probe  
2 comprises a base sequence derived from a fully defined sequence of 1227  
2 nucleotides as given in the specification and being labelled at the 3' or  
2 5' end with a fluorescent dye. The probe of the invention may be useful  
2 for detecting a mutation or single nucleotide polymorphism (SNP) in the  
2 beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
2 detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
2 contamination of the amplified product is prevented and the process is  
2 automated. The current sequence is that of the human beta3 adrenaline  
2 receptor (B3AR) T190 variant DNA fragment of the invention.

2 Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAGAC 20  
|||  
2 12 CATCGCCTGGACTCCGAGAC 31

RESULT 4  
AA04696

2 AAA04696 standard; DNA; 29 BP.

2 AAA04696;

2 22-MAY-2000 (first entry)

2 Polymorphic fragment of hypertension associated gene ADRB3.

2 Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
2 Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
2 Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;  
2 polycystic kidney disease; von Willebrands disease; forensic; human;  
2 tuberous sclerosis; hereditary hemorrhagica telangiectasia;  
2 familial colonic polyposis; osteogenesis imperfecta; porphyria;  
2 Ehlers-Danlos syndrome; ss.

2 Homo sapiens.

2 EP955382-A2.

2 10-NOV-1999.

2 07-MAY-1999; 99EP-00250150.

2 07-MAY-1998; 98US-0084641P.

2 03-MAY-1999; 99US-00304232.

2 (AFFY-) AFFYMETRIX INC.

2 (UYCA-) UNIV CASE WESTERN RESERVE.

2 Fan JB, Chakravarti A, Haluska MK;

2 WPI; 2000-107928/10.

2 Novel nucleic acids containing polymorphisms used in the diagnosis of  
2 hypertension.

2 Disclosure; Page 45; 53pp; English.

the invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 3; Length 29;  
Best Local Similarity 95.0%; Pred. No. 9.4;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAGAC 20  
|||||||:|||||||  
8 CATGCCYGGACTCCGAGAC 27

ESULT 5  
BK50101

ABK50101 standard; DNA; 41 BP.  
ABK50101;  
15-JUL-2002 (first entry)  
Nucleic acid sequence used for sequence formatting.  
Optimal reagent oligonucleotide; target nucleic acid evaluation;  
target feature; exclusion value; ranking value; sequence window;  
sequence formatting; ds.  
Synthetic.  
WO200229379-A2.  
11-APR-2002.  
04-OCT-2001; 2001WO-US031037.  
04-OCT-2000; 2000US-0237383P.  
(CELA-) CELADON LAB INC.  
Peterson RJ;  
WPI; 2002-340129/37.  
Determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature, involves defining a set of exclusion values and/or ranking values specific to a biochemical method.  
Example; Fig 1B; 91pp; English.  
The present invention relates to a new method for determining an optimal reagent oligonucleotide for evaluating a target nucleic acid having a target feature. The method comprises defining a set of exclusion values and/or ranking values specific to the method, defining a sequence window

adjacent to the target, and generating candidate reagent oligonucleotides complementary to the sense and/or antisense strands of the target within the window. The method can be used for determining an optimal reagent oligonucleotide sequence for use in a biochemical method for evaluating a target nucleic acid sequence having a target feature. The present nucleic acid sequence represent a DNA molecule used in the methods of the invention for nucleic acid sequence formatting

Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 6; Length 41;  
Best Local Similarity 95.0%; Pred. No. 9.6;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAGAC 20  
|||||||:|||||||  
14 CATGCCYGGACTCCGAGAC 33

RESULT 6  
D026526

ADO26526 standard; DNA; 25 BP.  
ADO26526;  
12-AUG-2004 (first entry)  
Novel hybridisation detection-related oligonucleotide SeqID2.  
hybridisation detection; immobilised probe; AC impedance;  
foetal genome analysis; ss.

Unidentified.  
WO2004044570-A1.  
27-MAY-2004.  
30-SEP-2003; 2003WO-JP012499.  
14-NOV-2002; 2002JP-00331059.  
(TOYA-) TOYAMA PREFECTURE.  
(COSE-) COSEL CO LTD.  
(TATE-) TATEYAMA KAGAKU IND CO LTD.  
(TOXX ) TOYO KAKO CO LTD.

Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;  
Nakagawa A, Mizuhara T, Mizushima M, Nakada M;  
WPI; 2004-420427/39.

Detection of hybridization of an immobilized probe to a target nucleic acid by measuring AC impedance across the carrier surface for specific gene detection in investigation and diagnosis of disease.

Example; SEQ ID NO 2; 33pp; Japanese.

This invention relates to a novel method of detecting hybridisation of an immobilised probe to a target nucleic acid using measurement of AC impedance. Detection of specific genes and gene sequences in nucleic acid samples (such as samples of genomic DNA) may be useful for diagnosis, prediction and prevention of genetic disorders and analysis of foetal genome. Hybridisation is detected with high accuracy and sensitivity without the use of dyes. The present sequence is that of an oligonucleotide which was used in the exemplification of the invention.

Sequence 25 BP; 4 A; 10 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 12; Length 25;  
Best Local Similarity 85.0%; Pred. No. 25.



Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAGAC 20  
||||||| |||||||||  
O 6 CATCGCCCGGACTCCGAGAC 25

ESULT 7  
DT93454  
O ADT93454 standard; DNA; 34 BP.  
K  
C ADT93454;  
K  
T 13-JAN-2005 (first entry)  
K  
E Human beta3 adrenaline receptor (B3AR) C190 variant DNA fragment.  
K  
W single nucleotide polymorphism; SNP; SNP detection;  
W beta3 adrenaline receptor; ds.  
K  
S Homo sapiens.  
K  
H Key Location/Qualifiers  
T variation replace(19,T)  
T /\*tag= a  
T /standard\_name= "Single nucleotide polymorphism"  
K  
N WO2004092385-A1.  
K  
O 28-OCT-2004.  
K  
F 16-APR-2004; 2004WO-JP005525.  
K  
R 18-APR-2003; 2003JP-00114381.  
K  
A (ARKR-) ARKRAY INC.  
K  
I Hirai M;  
K  
R WPI; 2004-784610/77.  
K  
T Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
T receptor gene having single nucleotide polymorphism, labeled at terminal  
T with fluorescent dye and shows decrease in fluorescence of fluorescent  
T dye upon hybridization.  
K  
S Example 1; Fig 1; 31pp; Japanese.  
K  
C The invention relates to a novel nucleic acid probe which is labelled at  
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
C of the fluorescent dye is observed upon hybridisation. The probe  
C comprises a base sequence derived from a fully defined sequence of 1227  
C nucleotides as given in the specification and being labelled at the 3' or  
C 5' end with a fluorescent dye. The probe of the invention may be useful  
C for detecting a mutation or single nucleotide polymorphism (SNP) in the  
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
C contamination of the amplified product is prevented and the process is  
C automated. The current sequence is that of the human beta3 adrenaline  
C receptor (B3AR) C190 variant DNA fragment of the invention.  
K  
Q Sequence 34 BP; 5 A; 14 C; 9 G; 6 T; 0 U; 0 Other;  
  
Query Match 92.0%; Score 18.4; DB 13; Length 34;  
Best Local Similarity 95.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAGAC 20  
||||||| |||||||||  
O 12 CATCGCCCGGACTCCGAGAC 31

ESULT 8

BK50104

D ABK50104 standard; DNA; 41 BP.

K

C ABK50104;

K

T 15-JUL-2002 (first entry)

K

E Sense strand of target nucleic acid.

K

W Optimal reagent oligonucleotide; target nucleic acid evaluation;  
W target feature; exclusion value; ranking value; sequence window;  
W single nucleotide polymorphism; SNP; ds.

K

S Synthetic.

K

H	Key	Location/Qualifiers
T	variation	replace(21,T)
T		/*tag= a
T		/standard_name= "Single nucleotide polymorphism"

K

N WO200229379-A2.

K

D 11-APR-2002.

K

F 04-OCT-2001; 2001WO-US031037.

K

R 04-OCT-2000; 2000US-0237383P.

K

A (CELA-) CELADON LAB INC.

K

I Peterson RJ;

K

R WPI; 2002-340129/37.

K

T Determining an optimal reagent oligonucleotide for evaluating a target  
T nucleic acid having a target feature, involves defining a set of  
T exclusion values and/or ranking values specific to a biochemical method.

K

S Example; Fig 4A; 91pp; English.

K

C The present invention relates to a new method for determining an optimal  
C reagent oligonucleotide for evaluating a target nucleic acid having a  
C target feature. The method comprises defining a set of exclusion values  
C and/or ranking values specific to the method, defining a sequence window  
C adjacent to the target, and generating candidate reagent oligonucleotides  
C complementary to the sense and/or antisense strands of the target within  
C the window. The method can be used for determining an optimal reagent  
C oligonucleotide sequence for use in a biochemical method for evaluating a  
C target nucleic acid sequence having a target feature. The present nucleic  
C acid sequence represent the sense strand of a target nucleic acid. This  
C sequence was used in the methods of the invention in a sequence window

K

Q Sequence 41 BP; 7 A; 16 C; 11 G; 7 T; 0 U; 0 Other;

Query Match	92.0%;	Score 18.4;	DB 6;	Length 41;
Best Local Similarity	95.0%;	Pred. No. 37;		
Matches	19;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;

Y	1	CATCGCCTGGACTCCGAGAC	20
O	14	CATCGCCCGGACTCCGAGAC	33

ESULT 9

DT93450

D ADT93450 standard; DNA; 18 BP.

K

C ADT93450;

V

1 15 JAN 2005 (first entry),  
X  
E Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.  
X  
W SNP detection; beta3 adrenaline receptor; ss; probe.  
X  
S Homo sapiens.  
X  
H Key Location/Qualifiers  
I modified\_base 1  
I /\*tag= a  
I /mod\_base= OTHER  
I /note= "OTHER = Linked to BODIPY FL group"  
I modified\_base 18  
I /\*tag= b  
I /mod\_base= OTHER  
I /note= "OTHER = Optionally linked to P group"  
X  
N WO2004092385-A1.  
X  
D 28-OCT-2004.  
X  
F 16-APR-2004; 2004WO-JP005525.  
X  
R 18-APR-2003; 2003JP-00114381.  
X  
A (ARKR-) ARKRAY INC.  
X  
I Hirai M;  
X  
R WPI; 2004-784610/77.  
X  
I Nucleic acid probe useful for detecting mutation in beta3 adrenaline  
I receptor gene having single nucleotide polymorphism, labeled at terminal  
I with fluorescent dye and shows decrease in fluorescence of fluorescent  
I dye upon hybridization.  
X  
S Claim 2; SEQ ID NO 10; 31pp; Japanese.  
X  
C The invention relates to a novel nucleic acid probe which is labelled at  
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence  
C of the fluorescent dye is observed upon hybridisation. The probe  
C comprises a base sequence derived from a fully defined sequence of 1227  
C nucleotides as given in the specification and being labelled at the 3' or  
C 5' end with a fluorescent dye. The probe of the invention may be useful  
C for detecting a mutation or single nucleotide polymorphism (SNP) in the  
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in  
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of  
C contamination of the amplified product is prevented and the process is  
C automated. The current sequence is that of the fluorescent-labelled probe  
C (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline  
C receptor (B3AR) T190 variant DNA.  
X  
2 Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 90.0%; Score 18; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 1 CATCGCCTGGACTCCGAG 18  
| | | | | | | | | | | | | | | |  
O 1 CATCGCCTGGACTCCGAG 18

ESULT 10  
EC91756/c  
D AEC91756 standard; DNA; 18 BP.  
X  
C AEC91756;  
X  
T 01 DEC 2005 (first entry)

E Probe 3T-B3AR-w-IMS-R1-18 SEQ ID NO:32.  
 X  
 W DNA detection; SNP detection; probe; ss.  
 K  
 S Synthetic.  
 K  
 N JP2005261354-A.  
 K  
 D 29-SEP-2005.  
 K  
 F 19-MAR-2004; 2004JP-00080974.  
 K  
 R 19-MAR-2004; 2004JP-00080974.  
 K  
 A (KYOT-) KYOTO DAIICHI KAGAKU KK.  
 K  
 I Inose K;  
 K  
 R WPI; 2005-662138/68.  
 K  
 T Detecting target nucleic acid, involves detecting target based on change  
 T of fluorescence intensity due to formation or dissociation of hybrid of  
 T target nucleic acid and hybridization probe having 5-carboxy fluorescein.  
 K  
 S Example 10; SEQ ID NO 32; 28pp; Japanese.  
 K  
 C The invention relates to a method (M1) for detecting a target nucleic  
 C acid. (M1) involves measuring the change of fluorescence intensity due to  
 C formation or dissociation of the hybrid of the hybridization probe  
 C comprising a labeled terminal portion, and a target nucleic acid, and  
 C detecting the target nucleic acid based on the change, where the  
 C hybridization probe is labeled using the fluorescent pigment chosen from  
 C 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora  
 C -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-  
 C dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),  
 C 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto  
 C hydrazide (Cascade blue). Also described: (1) a real-time PCR method  
 C (M2), which involves carrying out real-time PCR using the hybridization  
 C probe labeled with the fluorescent pigment, where the hybridization probe  
 C is the probe labeled at its terminal with the fluorescent pigment chosen  
 C from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-  
 C curve analysis (M3), which involves using the hybridization probe labeled  
 C with the fluorescent pigment, where the hybridization probe is the probe  
 C labeled at its terminal with the fluorescent pigment chosen from TAMRA,  
 C BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a  
 C target nucleic acid. (M1)-(M3) are useful for detecting mutations in a  
 C target nucleic acid and single nucleotide polymorphisms (SNPs), and in  
 C measurement of the ratio of normal type DNA and variant DNA. (M1) enables  
 C detection of the nucleic acid by fluorescent detection method, easily and  
 C cost effectively. The present sequence represents a probe used in an  
 C example from the present invention.  
 K  
 2 Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 14; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 ATCGCCTGGACTCCGAGA 19  
 |||||  
 18 ATCGCCTGGACTCCGAGA 1

ESULT 11  
 AF96886  
 AAF96886 standard; DNA; 21 BP.

AAF96886;  
 18 NOV 2004 (revised)

Human gene single nucleotide polymorphism #1647.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.

Homo sapiens.  
Unidentified.

Key	Location/Qualifiers
variation	11
	/*tag= a
	/standard_name= "Single nucleotide polymorphism"

WO200118250-A2.

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.  
26-JUL-2000; 2000US-0220947P.  
16-AUG-2000; 2000US-0225724P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.  
(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;  
WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.

Example; Page 159; 242pp; English.

The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPs shown in the specification

Revised record issued on 18-NOV-2004 : The variation feature was incorrectly given a capital V

Sequence 21 BP; 3 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 90.40%; Score 18; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

3 TCGCCTGGACTCCGAGAC 20
  |||||
1 TCGCCTGGACTCCGAGAC 18

```

18-NOV-2004 (revised)  
06-JUN-2001 (first entry)

Human gene single nucleotide polymorphism #1646.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
polymorphism; vascular disease; coronary artery disease; forensics;  
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
pulmonary embolism; paternity test; ds.

Homo sapiens.  
Unidentified.

Key	Location/Qualifiers
variation	11
	/*tag= a
	/standard_name= "Single nucleotide polymorphism"

WO200118250-A2.

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.

26-JUL-2000; 2000US-0220947P.

16-AUG-2000; 2000US-0225724P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.  
(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;

WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in  
applications such as forensics, paternity testing, medicine, genetic  
analysis and phenotype correlations to diseases such as diabetes and  
atherosclerosis.

Example; Page 159; 242pp; English.

The present invention provides a method of diagnosing a vascular disease  
in an individual, involving determining the sequence at various  
polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
genes. The sequences at a number of polymorphic sites are also provided  
in the specification. In particular, the method can be used in the  
diagnosis of atherosclerosis, myocardial infarction, coronary heart  
disease, stroke, peripheral vascular diseases, venous thromboembolism and  
pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
useful in forensics, paternity testing, genetic analysis and phenotype  
correlations to diseases. The present sequence is an example of one of  
the human gene SNPS shown in the specification

Revised record issued on 18-NOV-2004 : The variation feature was  
incorrectly given a capital V

Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18

|||||||

4 CATCGCCTGGACTCCGAG 21

ABL40567 standard; DNA; 26 BP.  
ABL40567;  
17-JUN-2002 (first entry)  
Primer #7 used in a base polymorphism detection method.  
Polymorphism; nucleic acid detection; endonuclease; probe; ADRB2;  
hybridisation; PCR primer; ss.  
Synthetic.  
JP2002034598-A.  
05-FEB-2002.  
27-JUL-2000; 2000JP-00226912.  
27-JUL-2000; 2000JP-00226912.  
(TOYM ) TOYOBO KK.  
WPI; 2002-298820/34.  
Detection of base polymorphism.  
Disclosure; Page 10; 10pp; Japanese.  
The invention relates to a method for detecting base polymorphism. The method involves (1) amplifying the nucleic acid fragment containing base polymorphism of the specific nucleic acid sequence; (2) hybridising the amplified nucleic acid with at least two polymorphism-specific probes; (3) treating with RNA-selective cleavage endonuclease; (4) measuring detecting signals of each probe; and (5) identifying polymorphism by the ratio of each detecting signals. The probe can be used for detecting base polymorphism. The present sequence represents a PCR primer used in the course of the invention  
Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATCGCCTGGACTCCGAG 18  
|||||||  
9 CATCGCCTGGACTCCGAG 26

ESULT 14  
AC73164

AAC73164 standard; DNA; 21 BP.  
AAC73164;  
02-FEB-2001 (first entry)  
SNP flanking sequence #24 used in multiplexing PCR/SBE assay.  
Oligonucleotide array; genotyping; single base extension reaction; SBE;  
polymorphic locus; single nucleotide polymorphism; ss.  
Unidentified.  
WO200058516-A2.  
05-OCT-2000.  
27 MAR 2000. 2000WO 05008050

R 26-MAR-1999; 99US-0126473P.  
R 23-JUN-1999; 99US-0140359P.  
X  
A (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
A (AFFY-) AFFYMETRIX INC.  
X  
I Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;  
I Ryder T, Sklar P;  
X  
R WPI; 2000-656171/63.  
X  
T Universal array of oligonucleotides tags attached to a solid substrate  
T along with locus-specific tagged oligonucleotides useful in genotyping  
T using single base extension reactions.  
X  
S Example 7; Page 50; 70pp; English.  
X  
C The present invention relates to an oligonucleotide array comprising  
C oligonucleotide tags fixed to a solid substrate. The oligonucleotide  
C array is useful for genotyping a nucleic acid sample at one or more loci



1:--StartFragment-->RESULT 1

3-09-304-232-896

Sequence 896, Application US/09304232

Patent No. 6525185

GENERAL INFORMATION:

APPLICANT: Fan, Jian Bing

APPLICANT: Chakravarti, Aravinda

APPLICANT: Halushka, Marc Kenneth

APPLICANT: Case Western Reserve University School of Medicine

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Polymorphisms Associated With

TITLE OF INVENTION: Hypertension

FILE REFERENCE: 018547-034210US

CURRENT APPLICATION NUMBER: US/09/304,232

CURRENT FILING DATE: 1999-05-03

EARLIER APPLICATION NUMBER: US 60/084,641

EARLIER FILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 909

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 896

LENGTH: 29

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: ADRB3EX1 416

3-09-304-232-896

Query Match 100.0%; Score 20; DB 3; Length 29;

Best Local Similarity 95.0%; Pred. No. 8.1;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CGTGGCCATCGCCCGGACTC 20

|||||||:|||||

2 CGTGGCCATCGCCYGGACTC 21

RESULT 2

3-08-891-516-39

Sequence 39, Application US/08891516

Patent No. 6090552

GENERAL INFORMATION:

APPLICANT: NAZARENKO, Irina A.

APPLICANT: BHATNAGAR, Satish K.

APPLICANT: WINN-DEEN, Emily S.

APPLICANT: HOHMAN, Robert J.

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

TITLE OF INVENTION: OLIGONUCLEOTIDES WITH MOLECULAR ENERGY TRANSFER LABELS AND

TITLE OF INVENTION: METHODS BASED THEREON

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/891,516

FILING DATE: 11-JUL-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/837,034

FILING DATE: 11-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/778,487

FILING DATE: 11-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,667

FILING DATE: 16-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 079498/0109

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-891-516-39

Query Match 85.0%; Score 17; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

y      1 CGTGGCCATCGCCCGGA 17
      ||||||||||||||||
o      11 CGTGGCCATCGCCCGGA 27
  
```

RESULT 3

3-08-837-034-39

Sequence 39, Application US/08837034

Patent No. 6117635

GENERAL INFORMATION:

APPLICANT: NAZARENKO, Irina A.

APPLICANT: BHATNAGAR, Satish K.

APPLICANT: WINN-DEEN, Emily S.

APPLICANT: HOHMAN, Robert J.

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

TITLE OF INVENTION: OLIGONUCLEOTIDES WITH MOLECULAR ENERGY TRANSFER LABELS AND

TITLE OF INVENTION: METHODS BASED THEREON

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/837,034

FILING DATE: 11-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/778,487

FILING DATE: 03-JAN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,667

FILING DATE: 16-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 079498/0110

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 39.

SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
S-08-837-034-39

Query Match 85.0%; Score 17; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CGTGGCCATCGCCCGGA 17  
|||||||  
o 11 CGTGGCCATCGCCCGGA 27

RESULT 4

S-09-657-472-1650

Sequence 1650, Application US/09657472

Patent No. 6727063

GENERAL INFORMATION:

APPLICANT: Lander, Eric S.

APPLICANT: Cargill, Michele

APPLICANT: Ireland, James S.

APPLICANT: Bolk, Stacey

APPLICANT: Daley, George Q.

APPLICANT: McCarthy, Jeanette J.

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

FILE REFERENCE: 2825.1027-001

CURRENT APPLICATION NUMBER: US/09/657,472

CURRENT FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/153,357

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US 60/220,947

PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: US 60/225,724

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2551

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1650

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

S-09-657-472-1650

Query Match 83.0%; Score 16.6; DB 3; Length 21;  
Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 4 GGCCATCGCCCGGACTC 20  
|||||||:|||||  
o 1 GGCCATCGCCYGGACTC 17

RESULT 5

S-08-891-516-38

Sequence 38, Application US/08891516

Patent No. 6090552

GENERAL INFORMATION:

APPLICANT: NAZARENKO, Irina A.

APPLICANT: BHATNAGAR, Satish K.

APPLICANT: WINN-DEEN, Emily S.

APPLICANT: HOHMAN, Robert J.

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

TITLE OF INVENTION: OLIGONUCLEOTIDES WITH MOLECULAR ENERGY TRANSFER LABELS AND

TITLE OF INVENTION: METHODS BASED THEREON

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 2000 K STREET N.W.

STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/891,516  
FILING DATE: 11-JUL-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/837,034  
FILING DATE: 11-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/778,487  
FILING DATE: 03-JAN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,667  
FILING DATE: 16-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 079498/0109

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-891-516-38

Query Match 77.0%; Score 15.4; DB 3; Length 27;  
Best Local Similarity 94.1%; Pred. No. 6.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CGTGGCCATCGCCCGGA 17  
          |||||||  
o 11 CGTGGCCATCGCCTGGA 27

ESULT 6  
!--EndFragment-->

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104357\_us-10-553-509- 1\_copy\_180\_240.rng.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104357\_us-10-53-509-1\_copy\_180\_240.rng.

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[Go Back to previous page](#)

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4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 14:32:10 ; Search time 299.969 Seconds  
(without alignments)  
1417.837 Million cell updates/sec

Title: US-10-553-509-1\_COPY\_180\_240  
Perfect score: 61  
Sequence: 1 ggccatcgccctggactccga.....tggtcgtgacttcgctggcc 61

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%				
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	61	100	0	1000	10	20061214_104357_us-10-553-509-1_copy_180_240.rng

2	61	100.0	1185	14	AEA13746	Aea13746 Human bet
3	61	100.0	1185	14	AEA13746	Aea13746 Human bet
4	61	100.0	1227	2	AAQ55693	Aaq55693 DNA encod
5	61	100.0	1227	13	ADT93441	Adt93441 Human bet
6	61	100.0	1270	10	ACA56586	Aca56586 Human sig
7	61	100.0	1270	12	ADI56382	Adi56382 Human pol
8	61	100.0	2022	2	AAQ05731	Aaq05731 Beta 3 ad
9	61	100.0	2518	2	AAV23500	Aav23500 Human adr
10	61	100.0	2644	8	ABZ42630	Abz42630 Human bet
11	61	100.0	2644	11	ADN39372	Adn39372 Cancer/an
12	61	100.0	2644	12	ADO29809	Ado29809 Human GPC
13	61	100.0	2644	13	ADU50894	Adu50894 Human bet
14	61	100.0	2644	14	AEC83014	Aec83014 Breast ca
15	61	100.0	2644	14	AEE01346	Aee01346 Human G p
16	61	100.0	3682	2	AAQ65476	Aaq65476 Human bet
17	61	100.0	5669	13	ADU50893	Adu50893 Human bet
18	60.6	100.0	210	2	AAX11762	Aax11762 Human bia
19	60.6	100.0	420	14	AEC91757	Aec91757 Template
20	60.6	100.0	5669	14	ADZ42281	Adz42281 Human bet
21	60.6	100.0	10306	6	ABK11451	Abk11451 Human bet
22	59.4	97.4	100	14	AEC91742	Aec91742 Template
23	59.4	97.4	210	2	AAX12815	Aax12815 Human bia
24	59.4	97.4	1227	13	ADT93442	Adt93442 Human bet
25	57.8	94.8	2000	2	AAQ74367	Aaq74367 Bovine be
26	51.4	84.3	2649	2	AAV30469	Aav30469 Canine be
27	50.4	82.6	1203	12	ADO30100	Ado30100 Mouse GPC
28	50.4	82.6	1920	2	AAQ26808	Aaq26808 Murine ad
29	50.4	82.6	3437	2	AAQ65477	Aaq65477 Murine be
30	44.6	73.1	704	6	ABQ50482	Abq50482 Oligonucl
31	44.6	73.1	704	6	ABQ50483	Abq50483 Oligonucl
32	44.6	73.1	5832	6	ABN80280	Abn80280 Human che
33	44.6	73.1	7431	6	ABL32081	Abl32081 Human imm
34	44.6	73.1	7431	6	AAD28371	Aad28371 Human che
35	42.6	69.8	75	10	ADD32083	Add32083 Human bet
36	42.2	69.2	75	10	ADD32073	Add32073 Human bet
37	41	67.2	75	10	ADD32084	Add32084 Human bet
38	40.6	66.6	2040	6	ABK11513	Abk11513 Human bet
39	38.6	63.3	4749	3	AAZ98401	Aaz98401 Sheep bet
40	38.6	63.3	4749	6	ABK40733	Abk40733 Sheep bet
41	37	60.7	1845	3	AAZ98400	Aaz98400 Canine be
42	37	60.7	1845	6	ABK40732	Abk40732 Dog beta1
43	36	59.0	1584	3	AAZ98406	Aaz98406 Frog beta
44	36	59.0	1584	6	ABK40738	Abk40738 Frog beta
45	35.4	58.0	704	6	ABQ50484	Abq50484 Oligonucl

ALIGNMENTS

ESULT 1  
 CH91802  
 D ACH91802 standard; DNA; 1003 BP.  
 X  
 C ACH91802;  
 X  
 T 29-JUL-2004 (first entry)  
 X  
 E Human genome derived single exon probe #24997.  
 X  
 W Human; probe; ss; gene expression; single exon probe; microarray;  
 W alternative splicing event; genomic alteration.  
 X  
 S Homo sapiens.  
 X  
 N US2003194704-A1.  
 X  
 D 16-OCT-2003.  
 X  
 F 03-APR-2002; 2002US-00029386.  
 X  
 D 02 APR 2002; 2002US 00029386



29-AUG-2003 (revised)  
28-MAY-2003 (first entry)

Human beta\_3AR-V2R DNA.

Human; G-protein coupled receptor; gene; ds; GPCR; palmitoylation site; phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis; atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain; rheumatoid arthritis; obesity; Parkinson's disease; beta\_3AR; V2R; vasopressin V2R receptor; beta3-adrenergic receptor.

Homo sapiens.  
Chimeric.

Key	Location/Qualifiers
CDS	1. .1185
	/*tag= a
	/product= "Human beta_3AR-V2R"

US2002106739-A1.

08-AUG-2002.

05-NOV-2001; 2001US-00993844.

03-NOV-2000; 2000US-0245772P.

08-JAN-2001; 2001US-0260363P.

(OAKL/) OAKLEY R H.  
(BARA/) BARAK L S.  
(LAPO/) LAPORTE S A.  
(CARO/) CARON M G.

Oakley RH, Barak LS, Laporte SA, Caron MG;

WPI; 2002-690758/74.

P-PSDB; ABG75678.

Modified G-protein coupled receptor useful for identifying an agonist, inverse agonist or antagonist of the receptor, comprises a carboxyl terminal having one or more clusters of phosphorylation.

Disclosure; Fig 11; 57pp; English.

The invention relates to a modified G-protein coupled receptor (GPCR) comprising an NPXXY motif, and a carboxyl terminal tail which comprises a putative site of palmitoylation and clusters of phosphorylation, and a retained portion of a carboxyl terminal region of a GPCR portion fused to a portion of the carboxyl terminal from a second GPCR, that comprises phosphorylation clusters and a putative palmitoylation site 10-25 amino acid residues downstream of a second NPXXY motif. The modified GPCR is useful for screening compounds for GPCR activity which comprises providing a cell that expresses at least one modified GPCR, where the cell further comprises arrestin conjugated to a detectable molecule, exposing the cell to the compound, detecting the location of the arrestin within the cell, comparing the location of the arrestin within the cell in the presence of the compound to the location of the arrestin within the cell in the absence of the compound and correlating a difference between the location of arrestin within the cell in the presence of the compound and the presence of the location of the arrestin within the cell in the absence of the compound. Preferably, the arrestin is detected in endosomes. The GPCR and a nucleic acid encoding the modified GPCR are useful for preventing and/or treating a disease associated with GPCR in mammals, such as angina pectoris, atherosclerosis, asthma, emphysema, rhinitis, inflammatory disease, rheumatoid arthritis, glaucoma, pain, obesity or Parkinson's disease, by modulating GPCR activity and affinity for arrestin. This sequence represents DNA encoding a chimeric receptor polypeptide used in the scope of the invention. (Updated on 29-AUG-2003 to standardize OS field)



```

2 Sequence 1185 BP; 132 A; 446 C; 371 G; 236 T; 0 U; 0 Other;
Query Match 100.0%; Score 61; DB 6; Length 1185;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
|||||
180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239
61 C 61
|
240 C 240

```

```

ESULT 3
EA13746
D AEA13746 standard; DNA; 1185 BP.
K
C AEA13746;
K
I 28-JUL-2005 (first entry)
K
E Human beta3AR - V2R chimeric DNA, SEQ ID NO: 13.
K
W G-protein coupled receptor; gpcr; neurodegenerative disease;
W neuroprotective; neurological disease; cardiovascular disease;
W cardiovascular-gen.; nephrotropic; genitourinary disease; antidiabetic;
W endocrine disease; gastrointestinal disease; metabolic disorder;
W antiinflammatory; inflammation; ophthalmological; ocular disease;
W gastrointestinal-gen.; analgesic; anorectic; nutritional disorder;
W eating-disorders-gen.; psychiatric disorder; antidepressant;
W tranquilizer; virucide; hematological disease; immune disorder;
W infection; cytostatic; neoplasm; gene therapy; vasopressin V2 receptor;
W beta 3 adrenoceptor; gene fusion; gene; ds.
K
S Homo sapiens.
K
H Key Location/Qualifiers
I CDS 1. .1185
I /*tag= a
I /product= "Beta3 adrenergic receptor-Vasopressin V2
I receptor fusion protein"
K
N US2005106623-A1.
K
D 19-MAY-2005.
K
F 30-DEC-2004; 2004US-00026435.
K
R 03-NOV-2000; 2000US-0245772P.
R 08-JAN-2001; 2001US-0260363P.
R 05-NOV-2001; 2001US-00993844.
K
A (OAKL/) OAKLEY R H.
A (BARA/) BARAK L S.
A (LAPO/) LAPORTE S A.
A (CARO/) CARON M G.
K
I Oakley RH, Barak LS, Laporte SA, Caron MG;
K
R WPI; 2005-365814/37.
R P-PSDB; AEA13740.
K
I Screening compounds for G-protein coupled receptor agonist or antagonist
I activity for preventing or treating, e.g. diabetes, comprises detecting
I location of arrestin in the cell in the presence and absence of the
I compound.
K
S Disclosure: SEQ ID NO 13. 87pp. English

```

3 The present invention relates to modified G-protein coupled receptor  
3 (GPCR) proteins and their encoding polynucleotides. The invention is  
3 useful in screening compounds for GPCR agonist or antagonist activity for  
3 preventing or treating diseases associated with GPCR in mammals such as  
3 neurodegenerative disorders, cardiovascular diseases such as angina  
3 pectoris, essential hypertension, myocardial infarction, atherosclerosis,  
3 renal failure, diabetes, respiratory indications, inflammatory disease,  
3 glaucoma, gastrointestinal indications, pain, obesity, bulimia nervosa,  
3 depression, obsessive-compulsive disorder, Epstein-Barr infection and  
3 cancer. The invention is also useful in gene therapy. The present  
3 sequence is human beta-3 adrenergic receptor (beta3AR) - vasopressin V2  
3 receptor (V2R) chimeric DNA. This chimeric DNA consists of the DNA  
3 encoding amino acids 1-363 of human beta3AR and amino acids 366-394 of  
3 human V2R.

X  
2 Sequence 1185 BP; 132 A; 446 C; 371 G; 236 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 14; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60  
|||  
O 180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239  
  
Y 61 C 61  
|  
O 240 C 240

RESULT 4  
AQ55693

O AAQ55693 standard; DNA; 1227 BP.

X  
C AAQ55693;

X  
T 25-MAR-2003 (revised)  
T 23-JUL-1994 (first entry)  
X

E DNA encoding the human beta-3 adrenergic receptor.

X  
W Fusion protein; compounds; ss.  
X

S Homo sapiens.  
X

N WO9402590-A1.  
X

O 03-FEB-1994.  
X

F 16-JUL-1993; 93WO-US006733.  
X

R 20-JUL-1992; 92US-00916901.  
X

A (UYWA-) UNIV WAYNE STATE.  
X

I Granneman JG, Lahners KN, Rao DD;  
X

R WPI; 1994-048848/06.  
R P-PSDB; AAR45740.  
X

T DNA encoding a beta 3-adrenergic receptor protein, opt. modified to avoid  
T fusion protein expression - can be used to identify cpds. which affect  
T receptor activity.  
X

S Claim 4; Fig 1; 80pp; English.  
X

C The human beta-3 adrenergic receptor protein is 408 amino acids long, not  
C 402 as previously reported, and is encoded as two introns. Host cells  
C expressing this DNA can be used to identify cpds. which affect the  
C activity of the receptor. Modifications in the DNA to mutate G1205 to T

protein. Oligonucleotide sequences which hybridise to this DNA may be used as probes to detect mRNA specific for beta-3 adrenergic receptor protein in cells. See also AAQ55694-707. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 1227 BP; 125 A; 465 C; 389 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 2; Length 1227;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
|||||
180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239

61 C 61
|
240 C 240
```

RESULT 5  
DT93441

ADT93441 standard; DNA; 1227 BP.

ADT93441;

13-JAN-2005 (first entry)

Human beta3 adrenaline receptor (B3AR) T190 variant DNA.

single nucleotide polymorphism; SNP; SNP detection;  
beta3 adrenaline receptor; ds.

Homo sapiens.

Key	Location/Qualifiers
variation	replace(190,C)
	/*tag= a
	/standard_name= "Single nucleotide polymorphism"

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 1; SEQ ID NO 1; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Tm64Aa mutation within a short time whilst risk of

contamination of the amplified product is prevented and the process is automated. The current sequence is that of the human beta3 adrenaline receptor (B3AR) T190 variant DNA of the invention.

\*Sequence 1227 BP; 125 A; 463 C; 391 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 13; Length 1227;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
|||||
180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

61 C 61
|
240 C 240
```

#### RESULT 6

CA56586

ACA56586 standard; cDNA; 1270 BP.

ACA56586;

06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1184.

Human; probe; ss; array element; Parkinson's disease;  
signalling pathway population; cancer; adenocarcinoma; leukaemia;  
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.

US6500938-B1.

31-DEC-2002.

30-JAN-1998; 98US-00016434.

30-JAN-1998; 98US-00016434.

(INCY-) INCYTE GENOMICS INC.

Au-Young J, Seilhamer JJ;

WPI; 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a  
microarray for monitoring the expression of a number of target  
polynucleotides.

Claim 1; SEQ ID NO 1184; 65pp; English.

The invention relates to a combination which, comprises a number of  
polynucleotide probes comprising a sequence selected from one of the 1490  
sequences mentioned in the specification. The combination is useful as an  
array element in a microarray for monitoring the expression of a number  
of target polynucleotides. The microarray is particularly useful in the  
diagnosis and treatment of cancer and immunopathology and neuropathology.  
The microarray is useful in diagnostics and treatment regimens, drug  
discovery and development, toxicological and carcinogenicity studies,  
forensics and pharmacogenomics. The microarray is also useful for  
monitoring progression of diseases and for developing sophisticated  
profiles for the effects of currently available therapeutic drugs. The  
combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
and genomic fragments and in research and diagnostic applications. The  
array can detect changes in expression in a large number of genes coding  
for different signaling pathway populations which can be used to diagnose  
various diseases including cancer e.g. adenocarcinoma and leukaemia

Immunopathology e.g. AIDS and asthma, neuropathology e.g. Alzheimer's disease  
and Parkinson's disease. The present sequence represents a polynucleotide  
probe of the invention. Note: The sequence data for this patent did not  
form part of the printed specification but was obtained in electronic  
format directly from USPTO at  
seqdata.uspto.gov/sequence.html?DocID=06500938B1

Sequence 1270 BP; 132 A; 484 C; 405 G; 249 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 10; Length 1270;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
217 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 276

61 C 61
   |
277 C 277
```

ESULT 7  
DI56382

ADI56382 standard; DNA; 1270 BP.

ADI56382;

22-APR-2004 (first entry)

Human polynucleotide probe #1184.

Human; probe; ss; receptor-like polypeptide; transducing polypeptide;  
effector-like polypeptide; cancer; immunopathology; neuropathology;  
drug development; toxicology; carcinogenicity;  
signalling pathway polypeptide; adrenal gland; bladder; bone;  
bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;  
dementia; amnesia; epilepsy; Alzheimer's disease; depression.

Homo sapiens.

US2004010136-A1.

15-JAN-2004.

26-NOV-2002; 2002US-00305720.

30-JAN-1998; 98US-00016434.

(INCY-) INCYTE GENOMICS INC.

Au-Young J, Seilhamer JJ;

WPI; 2004-090520/09.

New composition comprising polynucleotide probes, useful as array  
elements in a microarray for monitoring the expression of target  
polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
fragments.

Claim 6; SEQ ID NO 1184; 73pp; English.

The invention relates to a composition of polynucleotide probes  
comprising first polynucleotide probes comprising at least a portion of a  
gene encoding a receptor-like polypeptide, second polynucleotide probes  
comprising at least a portion of a gene encoding a transducing  
polypeptide and third polynucleotide probes comprising at least a portion  
of a gene encoding an effector-like polypeptide. The probes of the  
composition are useful as array elements in a microarray for monitoring  
the expression of target polynucleotides. The microarray is useful in the

diagnosis and treatment of cancer, an immunopathology, or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, amnesia, epilepsy, Alzheimer's disease or depression. This sequence represents a human polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 1270 BP; 132 A; 484 C; 405 G; 249 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 12; Length 1270;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60  
|||||  
217 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 276  
  
61 C 61  
|  
277 C 277

RESULT 8  
AAQ05731

AAQ05731 standard; DNA; 2022 BP.

AAQ05731;

25-MAR-2003 (revised)  
07-JAN-1991 (first entry)

Beta 3 adrenergic receptor gene.

Beta 3 adrenergic receptor gene; lipolysis; insulin; drugscreening; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	638..1844
	/*tag= a
	/product= "beta 3 adrenergic receptor"

WO9008775-A.

09-AUG-1990.

25-JAN-1989; 89FR-00000918.

25-JAN-1989; 89FR-00000918.

(CNRS ) CNRS CENT NAT RECH SCI.  
(INSP ) INST PASTEUR.

Emorine L, Rullo S, Strosberg D;

WPI; 1990-260892/34.  
P-PSDB; AAR06495.

New beta 3 adrenergic receptor polypeptide and encoding nucleic acid - involved in lipolysis, insulin secretion, etc. useful for screening drugs to control these processes

3 Disclosure; Fig 1bis; 51pp; French.  
 X  
 C The gene has been identified in a human genomic bank by screening with  
 C (a) the gene for turkey beta 1 receptor and (b) the gene for human beta 2  
 C receptor. Clones contg. an intron-free gene with better than 40% homology  
 C with the beta 1/2 genes were found and designated beta 3 receptor.  
 E Vectors for expression of this gene are plasmids, cosmids or phages, esp.  
 C the phage M13mp18-Hubeta3 (CNCM I-883), and these are used to transform  
 C bacteria or eukaryotic cells. The peptide is implicated in the lipolytic  
 C response of adipose tissue, in insulin secretion and in intestinal  
 C relaxation. It is useful for screening compounds which can act as specific  
 C ligands, i.e. potentially suitable as drugs for treatment of obesity,  
 C diabetes and hyperlipidaemia. (Updated on 25-MAR-2003 to correct PA  
 C field.)  
 X  
 2 Sequence 2022 BP; 282 A; 679 C; 644 G; 414 T; 0 U; 3 Other;

Query Match 100.0%; Score 61; DB 2; Length 2022;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60  
 C ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 C 817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 876  
 Y 61 C 61  
 C |  
 C 877 C 877

ESULT 9  
 AV23500  
 C AAV23500 standard; cDNA; 2518 BP.  
 X  
 C AAV23500;  
 X  
 T 28-JUL-1998 (first entry)  
 X  
 E Human adrenaline beta-receptor nucleotide sequence.  
 X  
 W Human adrenilin beta-receptor; uncoupling protein; UCP; adipocyte;  
 W metabolism; obesity; ss.  
 X  
 S Homo sapiens.  
 X  
 H Key Location/Qualifiers  
 T CDS 102..1329  
 T /\*tag= a  
 T /product= "human adrenaline beta-receptor product"  
 X  
 N JP10033178-A.  
 X  
 C 10-FEB-1998.  
 X  
 F 23-JUL-1996; 96JP-00193537.  
 X  
 R 23-JUL-1996; 96JP-00193537.  
 X  
 A (KAOS ) KAO CORP.  
 X  
 R WPI; 1998-172096/16.  
 R P-PSDB; AAW53847.  
 X  
 T Preparing cultured cells capable of converting into adypocytes - by  
 T transferring cells with human adrenalin beta receptor and un-coupling  
 T protein.  
 X  
 S Example 1; Fig 1; 8pp; Japanese.  
 X  
 C This is the nucleotide sequence for the human adrenilin beta receptor. In

the presence of the uncoupling protein (UCP), capable of differentiating or converting into adipocytes. The cells may be used for the analysis of intracellular information transfer and energy metabolism, and development of compositions for the analysis and control of these systems. The cells can also be used for the prevention and treatment of obesity

2. Sequence 2518 BP; 393 A; 824 C; 699 G; 602 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 2; Length 2518;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60  
|||||  
282 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 341  
61 C 61  
|  
342 C 342

ESULT 10

3Z42630

ABZ42630 standard; DNA; 2644 BP.

ABZ42630;

04-MAR-2003 (first entry)

Human beta-3 adrenoceptor nucleotide SEQ ID NO:53.

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
G protein-coupled receptor modulator; antibody; immune-related disease;  
growth-related disease; cell regeneration-related disease; AIDS; cancer;  
immunological-related cell proliferative disease; autoimmune disease;  
Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
ulcer; gene; ds.

Homo sapiens.

WO200261087-A2.

08-AUG-2002.

19-DEC-2001; 2001WO-US050107.

19-DEC-2000; 2000US-0257144P.

(LIFE-) LIFESPAN BIOSCIENCES INC.

Burmer GC, Roush CL, Brown JP;

WPI; 2003-046718/04.

P-PSDB; ABP81786.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein coupled receptor (GPCR) or a candidate polypeptide in a sample.



and (2), an isolated antibody, having high specificity and high affinity, of avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 2644 BP; 422 A; 856 C; 741 G; 625 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 8; Length 2644;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60  
|||||  
377 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 436  
  
61 C 61  
|  
437 C 437

ESULT 11  
DN39372

ADN39372 standard; cDNA; 2644 BP.  
ADN39372;  
17-JUN-2004 (first entry)  
Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B56.  
Human; differential expression; cancer; angiogenic disorder;  
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
inflammatory disease; autoimmune disease;  
retinal neovascularistaion syndrome; scarring; uterine fibroid;  
detection; diagnosis; prognosis; drug screening; drug targeting;  
wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
vulnerary; gene therapy; vaccine; gene; ss.  
Homo sapiens.  
WO2003042661-A2.  
22-MAY-2003.  
13-NOV-2002; 2002WO-US036810.  
13-NOV-2001; 2001US-0350666P.  
21-NOV-2001; 2001US-0332464P.  
29-NOV-2001; 2001US-0334393P.  
03-DEC-2001; 2001US-0335394P.  
14-DEC-2001; 2001US-0340376P.  
08-JAN-2002; 2002US-0347211P.  
10-JAN-2002; 2002US-0347349P.  
08 FEB 2002; 2002US 0355250P

20-FEB-2002; 2002US-0359077P.  
29-MAR-2002; 2002US-0368809P.  
04-APR-2002; 2002US-0370110P.  
12-APR-2002; 2002US-0372246P.  
05-JUN-2002; 2002US-0386614P.  
16-JUL-2002; 2002US-0396839P.  
22-JUL-2002; 2002US-0397775P.  
22-JUL-2002; 2002US-0397845P.  
09-SEP-2002; 2002US-0409450P.

(EOSB-) EOS BIOTECHNOLOGY INC.

Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;  
Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
WPI; 2003-468649/44.  
P-PSDB; ADN39373.

Determining the presence or absence of a pathological cell in a patient,  
useful for diagnosing, prognosing or treating cancer, comprises detecting  
a nucleic acid in a biological sample.

Claim 8; SEQ ID NO B56; 1385pp; English.

The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
whose expression is upregulated or downregulated in specific cancers or  
other diseases such as angiogenic or fibrotic disorders, and to methods  
of determining the presence or absence of a pathological cell in a  
patient by detecting a nucleic acid at least 80% identical to those of  
the invention or by detecting a polypeptide of the invention. The  
invention also relates to expression vectors and host cells comprising a  
nucleic acid of the invention; antibodies which specifically bind a  
polypeptide of the invention; use of such antibodies for drug targeting;  
and methods of screening for modulators of activity or expression of the  
polypeptides and nucleic acids. The nucleic acids, polypeptides,  
antibodies and methods are useful for diagnosing, prognosing and treating  
cancer and other conditions such as psoriasis, ischaemia, heart disease,  
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
neovascularisation syndromes, scarring and uterine fibroids. They may  
also be useful in wound healing and in contraception. The present  
sequence represents a nucleic acid sequence of the invention.

Sequence 2644 BP; 422 A; 856 C; 741 G; 625 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 11; Length 2644;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
|||||
377 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 436

61 C 61
|
437 C 437
```

ESULT 12  
DO29809  
ADO29809 standard; cDNA; 2644 BP.  
ADO29809;  
29-JUL-2004 (first entry)  
Human GPCR ADRB3 polynucleotide, SEQ ID NO:911.  
G protein-coupled receptor; GPCR; drug screening; diagnosis;  
transgenic mouse; neurological disorder; adrenal gland disorder;  
colon disorder; intestinal disorder; cardiovascular disorder.

.  
N joint disorder; metabolic disorder; nutritive disorder; cancer;  
N kidney disorder; liver disorder; lung disorder; breast disorder;  
N ovary disorder; uterus disorder; prostate disorder; testis disorder;  
N skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
N thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
N cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
N CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
N virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
N dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
N immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
N gene; ss.  
X  
S Homo sapiens.  
X  
N WO2004040000-A2.  
X  
D 13-MAY-2004.  
X  
F 09-SEP-2003; 2003WO-US028226.  
X

# SCORE Search Results Details for Application 10553509 and Search Result 20061214\_104404\_us-10-553-509- 1\_copy\_180\_240.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10553509 and Search Result 20061214\_104404\_us-10-53-509-1\_copy\_180\_240.rni.

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

4 nucleic - nucleic search, using sw model

Run on: December 15, 2006, 15:53:11 ; Search time 152.186 Seconds  
(without alignments)  
749.990 Million cell updates/sec

Title: US-10-553-509-1\_COPY\_180\_240  
Perfect score: 61  
Sequence: 1 ggccatcgccctggactccga.....tggtcgtgacttcgctggcc 61

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	61	100.0	1134	2	US-08-087-772A-14	Sequence 14, Appl
2	61	100.0	1185	5	US-09-993-844A-13	Sequence 13, Appl
3	61	100.0	1227	2	US-07-916-901-1	Sequence 1, Appli
4	61	100.0	1227	2	US-08-351-473B-7	Sequence 7, Appli
5	61	100.0	1270	3	US-09-016-434-1184	Sequence 1184, Ap
6	61	100.0	2602	2	US-02-452-862-1	Sequence 1, Appli

8	61	100.0	3683	3	US-09-895-211-1	Sequence 1, Appli
9	57.8	94.8	1218	2	US-08-351-473B-6	Sequence 6, Appli
10	57.8	94.8	2000	2	US-08-351-473B-1	Sequence 1, Appli
11	50.4	82.6	298	2	US-08-087-772A-7	Sequence 7, Appli
12	50.4	82.6	1164	2	US-08-087-772A-3	Sequence 3, Appli
13	50.4	82.6	1360	2	US-08-087-772A-4	Sequence 4, Appli
14	50.4	82.6	1920	2	US-08-087-772A-1	Sequence 1, Appli
15	50.4	82.6	2005	2	US-07-916-901-5	Sequence 5, Appli
16	50.4	82.6	3437	3	US-08-450-962-3	Sequence 3, Appli
17	50.4	82.6	3437	3	US-08-848-631-3	Sequence 3, Appli
18	50.4	82.6	3437	3	US-09-895-211-3	Sequence 3, Appli
19	38.6	63.3	4749	3	US-09-614-034-189	Sequence 189, App
20	37	60.7	1845	3	US-09-614-034-188	Sequence 188, App
21	36	59.0	1584	3	US-09-614-034-194	Sequence 194, App
22	35.4	58.0	1525	3	US-09-614-034-193	Sequence 193, App
23	35.4	58.0	1723	3	US-09-614-034-187	Sequence 187, App
24	35.4	58.0	1723	3	US-09-016-434-1182	Sequence 1182, Ap
25	35.4	58.0	4401	3	US-09-614-034-192	Sequence 192, App
26	28	45.9	1113	5	US-09-993-844A-9	Sequence 9, Appli
27	28	45.9	1242	7	PCT-US91-00909-3	Sequence 3, Appli
28	28	45.9	2305	3	US-09-016-434-1282	Sequence 1282, Ap
29	28	45.9	2305	3	US-09-023-655-1249	Sequence 1249, Ap
30	28	45.9	2340	3	US-09-856-803-1	Sequence 1, Appli
31	28	45.9	3451	3	US-09-811-286-1	Sequence 1, Appli
32	25.4	41.6	1254	7	PCT-US91-00909-1	Sequence 1, Appli
33	24.6	40.3	29	3	US-09-304-232-896	Sequence 896, App
34	24	39.3	1368	3	US-09-906-408A-4	Sequence 4, Appli
35	23.8	39.0	525	3	US-09-252-991A-14501	Sequence 14501, A
36	23.8	39.0	903	3	US-09-252-991A-10886	Sequence 10886, A
37	23.8	39.0	1035	4	US-10-324-967-11	Sequence 11, Appl
38	23.8	39.0	1092	3	US-09-252-991A-14759	Sequence 14759, A
39	23.8	39.0	1158	3	US-09-252-991A-10906	Sequence 10906, A
40	23.8	39.0	1305	3	US-09-252-991A-10830	Sequence 10830, A
41	23.8	39.0	2145	3	US-09-252-991A-14638	Sequence 14638, A
42	23.8	39.0	2487	3	US-09-252-991A-14985	Sequence 14985, A
43	23.8	39.0	3450	3	US-09-902-540-9001	Sequence 9001, Ap
44	23.8	39.0	7305	3	US-09-902-540-961	Sequence 961, App
45	23.4	38.4	1242	3	US-09-489-039A-5521	Sequence 5521, Ap

# ALIGNMENTS

ESULT 1  
3-08-087-772A-14  
Sequence 14, Application US/08087772A  
Patent No. 5691155  
GENERAL INFORMATION:  
APPLICANT: Nahmias, Clara  
APPLICANT: Emorine, Jean L.  
APPLICANT: Strosberg, Donny A.  
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine  
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5691155th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,772A  
FILING DATE:  
CLASSIFICATION: 800

GENERAL INFORMATION:

NAME: Linker, Raymond O.  
 REGISTRATION NUMBER: 26,419  
 REFERENCE/DOCKET NUMBER: 3339-195

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-881-3140  
 TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

S-08-087-772A-14

Query Match 100.0%; Score 61; DB 2; Length 1134;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-13;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
          |||
o          180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239

y          61 C 61
          |
o          240 C 240
  
```

RESULT 2

S-09-993-844A-13

Sequence 13, Application US/09993844A  
 Patent No. 7018812

GENERAL INFORMATION:

APPLICANT: Oakley, Robert H.  
 APPLICANT: Barak, Lawrence S.  
 APPLICANT: Laporte, Stephane A.  
 APPLICANT: Caron, Marc G.  
 TITLE OF INVENTION: Modified G-Protein Coupled Receptors  
 FILE REFERENCE: 033072-026  
 CURRENT APPLICATION NUMBER: US/09/993,844A  
 CURRENT FILING DATE: 2001-11-05  
 PRIOR APPLICATION NUMBER: US 60/245,772  
 PRIOR FILING DATE: 2000-11-03  
 PRIOR APPLICATION NUMBER: US 60/260,363  
 PRIOR FILING DATE: 2001-01-08  
 NUMBER OF SEQ ID NOS: 82  
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 1185

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: nucleotide sequence of beta3-AR-V2R chimera

S-09-993-844A-13

Query Match 100.0%; Score 61; DB 5; Length 1185;  
 Best Local Similarity 100.0%; Pred. No. 8e-13;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
          |||
o          180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239

y          61 C 61
          |
o          240 C 240
  
```

RESULT 3

S-07-016-001-1

GENERAL INFORMATION:

APPLICANT: Granneman, James G.  
APPLICANT: Lahners, Kristine N.  
APPLICANT: Rao, Donald D.  
TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA  
TITLE OF INVENTION: ENCODING SAME  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &  
ADDRESSEE: MILTON  
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390  
CITY: Troy  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/916,901  
FILING DATE: 19920720  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-324 (WSU)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1227 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS  
LOCATION: 1..1224

3-07-916-901-1

Query Match 100.0%; Score 61; DB 2; Length 1227;  
Best Local Similarity 100.0%; Pred. No. 8.1e-13;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
            |||
o          180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239

y          61 C 61
            |
o          240 C 240
```

ESULT 4  
3-08-351-473B-7  
Sequence 7, Application US/08351473B  
Patent No. 5656440  
GENERAL INFORMATION:  
APPLICANT: LENZEN, GERLINDA  
APPLICANT: KAPOOR, ARCHANA  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE  
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON

NAME: VANDERKAM

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/351,473B

FILING DATE: 21-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 93 04670

FILING DATE: 21-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR94/00447

FILING DATE: 21-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 6639-001-0X PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1227 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-351-473B-7

Query Match 100.0%; Score 61; DB 2; Length 1227;  
Best Local Similarity 100.0%; Pred. No. 8.1e-13;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
O          180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239

Y          61 C 61
          |
O          240 C 240
```

RESULT 5

3-09-016-434-1184

Sequence 1184, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:



REGISTRATION NUMBER: 08/09/1993

FILING DATE: HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1184:

SEQUENCE CHARACTERISTICS:

LENGTH: 1270 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g178895

3-09-016-434-1184

Query Match 100.0%; Score 61; DB 3; Length 1270;  
Best Local Similarity 100.0%; Pred. No. 8.1e-13;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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y      1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o      217 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 276

y      61 C 61
      |
o      277 C 277
```

RESULT 6

3-08-450-962-1

Sequence 1, Application US/08450962

Patent No. 6274706

GENERAL INFORMATION:

APPLICANT: EMORINE, Laurent; MARULLO, Stefano;

APPLICANT: STROSBERG, Donny

TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND

TITLE OF INVENTION: GENES

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: KECK, MAHIN & CATE

STREET: P.O. BOX 06110

CITY: CHICAGO

STATE: ILLINOIS

COUNTRY: U.S.A.

ZIP: 60606-0110

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/2" diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,962

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,829

FILING DATE: 08-SEPT-1993

APPLICATION NUMBER: 07/721,571

FILING DATE: 25-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,829

FILING DATE: 25 JUN 1999

ATTORNEY/AGENT INFORMATION:

NAME: Fleit, Martin; Gollin, Michael A.

REGISTRATION NUMBER: 16,900; 31,957

REFERENCE/DOCKET NUMBER: 47078-042

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 789-3400

TELEFAX: (202) 789-1158

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3683 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

3-08-450-962-1

Query Match 100.0%; Score 61; DB 3; Length 3683;

Best Local Similarity 100.0%; Pred. No. 1e-12;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
y      1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o      817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 876

y      61 C 61
      |
o      877 C 877
```

RESULT 7

3-08-848-631-1

Sequence 1, Application US/08848631

Patent No. 6635442

GENERAL INFORMATION:

APPLICANT: EMORINE, Laurent; MARULLO, Stefano;  
STROSBERG, Donny

TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND  
MOUSE  $\alpha$ 3-ADRENERGIC RECEPTOR  
GENES

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: KECK, MAHIN & CATE

STREET: P.O. BOX 06110

CITY: CHICAGO

STATE: ILLINOIS

COUNTRY: U.S.A.

ZIP: 60606-0110

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/2" diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/848,631

FILING DATE: 08-Jun-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/721,571

FILING DATE: 25-MAY-1990

APPLICATION NUMBER: PCT/FR89/00918

FILING DATE: 25-JAN-1989

ATTORNEY/AGENT INFORMATION:

NAME: Fleit, Martin; Gollin, Michael A.

REGISTRATION NUMBER: 16,900; 31,957

REFERENCE/DOCKET NUMBER: 47078-042

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 789-3400

TELEFAX: (202) 789-1158

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3683 bases

TYPE: nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

3-08-848-631-1

Query Match 100.0%; Score 61; DB 3; Length 3683;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60  
|||||  
817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 876  
61 C 61  
|  
877 C 877

RESULT 8

3-09-895-211-1

Sequence 1, Application US/09895211

Patent No. 6949636

GENERAL INFORMATION:

APPLICANT: Hunton and Williams

APPLICANT: Emorine, Laurent

TITLE OF INVENTION: INTRON/EXON STRUCTURE OF THE HUMAN AND MOUSE BETA3 ADRENERGIC RECEPTOR

TITLE OF INVENTION: GENES

FILE REFERENCE: 58769.000011

CURRENT APPLICATION NUMBER: US/09/895,211

CURRENT FILING DATE: 2001-07-02

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 3683

TYPE: DNA

ORGANISM: Homo sapiens

3-09-895-211-1

Query Match 100.0%; Score 61; DB 3; Length 3683;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60  
|||||  
817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 876  
61 C 61  
|  
877 C 877

RESULT 9

3-08-351-473B-6

Sequence 6, Application US/08351473B

Patent No. 5656440

GENERAL INFORMATION:

APPLICANT: LENZEN, GERLINDA

APPLICANT: KAPOOR, ARCHANA

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE

TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/351,473B

FILING DATE: 21-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 93 04670

FILING DATE: 21-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR94/00447

FILING DATE: 21-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 6639-001-0X PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-351-473B-6

Query Match 94.8%; Score 57.8; DB 2; Length 1218;  
Best Local Similarity 96.7%; Pred. No. 1.2e-11;  
Matches 59; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 60
          |||
o          180 GGCCATCGCCCGGACGCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGC 239

y          61 C 61
          |
o          240 C 240
    
```

RESULT 10

3-08-351-473B-1

Sequence 1, Application US/08351473B

Patent No. 5656440

GENERAL INFORMATION:

APPLICANT: LENZEN, GERLINDA

APPLICANT: KAPOOR, ARCHANA

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE

TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/351,473B

FILING DATE: 21-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 93 04670

FILING DATE: 21 APR 1993

SEQUENCE INFORMATION:

APPLICATION NUMBER: PCT/FR94/00447

FILING DATE: 21-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 6639-001-0X PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2000 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 107..1321

OTHER INFORMATION: /function= "BOVINE BETA-3 RECEPTOR"

OTHER INFORMATION: /product= "ADRENERGIC, BETA RECEPTOR"

3-08-351-473B-1

Query Match 94.8%; Score 57.8; DB 2; Length 2000;  
Best Local Similarity 96.7%; Pred. No. 1.4e-11;  
Matches 59; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60  
|||||  
286 GGCCATCGCCCGACGCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 345  
61 C 61  
|  
346 C 346

RESULT 11

3-08-087-772A-7

Sequence 7, Application US/08087772A

Patent No. 5691155

GENERAL INFORMATION:

APPLICANT: Nahmias, Clara

APPLICANT: Emorine, Jean L.

APPLICANT: Strosberg, Donny A.

TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine

TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bell, Seltzer, Park & Gibson

STREET: Post Office Drawer 34009

CITY: Charlotte

STATE: No. 5691155th Carolina

COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/087,772A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Linker, Raymond O.

REGISTRATION NUMBER: 26,419

REFERENCE/DOCKET NUMBER: 3339-195

TELECOMMUNICATION INFORMATION:

TELEPHONE: 010 001 2140

2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGCC 61  
 |||||  
 172 GCCATCGCCCGCACGCCGAGACTACAGACCATAACCAACGTGTTTCGTGACTTCAGTGGCC 231

3-08-087-772A-4  
Sequence 4, Application US/08087772A  
Patent No. 5691155

GENERAL INFORMATION:

APPLICANT: Nahmias, Clara  
APPLICANT: Emorine, Jean L.  
APPLICANT: Strosberg, Donny A.  
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine  
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5691155th Carolina  
COUNTRY: USA  
ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/087,772A  
FILING DATE:  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Linker, Raymond O.  
REGISTRATION NUMBER: 26,419  
REFERENCE/DOCKET NUMBER: 3339-195

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

3-08-087-772A-4

Query Match 82.6%; Score 50.4; DB 2; Length 1360;  
Best Local Similarity 90.0%; Pred. No. 6.5e-09;  
Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTCGTGACTTCGCTGGCC 61  
||||||| | || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
185 GCCATCGCCCGACGCCGAGACTACAGACCATAACCAACGTGTCGTGACTTCACTGGCC 244

ESULT 14  
3-08-087-772A-1  
Sequence 1, Application US/08087772A  
Patent No. 5691155

GENERAL INFORMATION:

APPLICANT: Nahmias, Clara  
APPLICANT: Emorine, Jean L.  
APPLICANT: Strosberg, Donny A.  
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine  
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5691155th Carolina  
COUNTRY: USA  
ZIP: 28234

COMPUTER READABLE FORM.

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/087,772A  
FILING DATE:  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Linker, Raymond O.  
REGISTRATION NUMBER: 26,419  
REFERENCE/DOCKET NUMBER: 3339-195

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1920 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS  
LOCATION: 568..1731

3-08-087-772A-1

Query Match 82.6%; Score 50.4; DB 2; Length 1920;  
Best Local Similarity 90.0%; Pred. No. 7.1e-09;  
Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTTCGTGACTTCGCTGGCC 61  
||||||| | || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||  
739 GCCATCGCCCGCACGCCGAGACTACAGACCATAACCAACGTGTTTCGTGACTTCACTGGCC 798

RESULT 15

3-07-916-901-5

Sequence 5, Application US/07916901  
Patent No. 5364772

GENERAL INFORMATION:

APPLICANT: Granneman, James G.  
APPLICANT: Lahners, Kristine N.  
APPLICANT: Rao, Donald D.  
TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA  
TITLE OF INVENTION: ENCODING SAME  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &  
ADDRESSEE: MILTON  
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390  
CITY: Troy  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/916,901  
FILING DATE: 19920720  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-324 (WSU)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

INFORMATION FOR SEQ ID NO: 5.



3-07-916-901-5

[illegible]

**tart**

SCORE 1.3    BuildDate: 11/17/2006